

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: INFECTIO DIAGNOSTIC (I.D.I.) INC.
(B) STREET: 2050, BOULEVARD RENE LEVSSQUE OUEST, 4E ETAGE
(C) CITY: STE-FOY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1V 2K8
(G) TELEPHONE: (418) 681-4343
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- (A) NAME: BERGERON, MICHEL G.
(B) STREET: 2069 RUE BRULARD
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
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- (A) NAME: PICARD, FRANCOIS J.
(B) STREET: 1245, RUE DE LA SAPINIERE
(C) CITY: CAP-ROUGE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1Y 1A1

- (A) NAME: OUELLETTE, MARC
(B) STREET: 1035 DE PLOERMEL
(C) CITY: SILLERY
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G1S 3S1

- (A) NAME: ROY, PAUL H.
(B) STREET: 28, RUE CHARLES GARNIER
(C) CITY: LORETTEVILLE
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) POSTAL CODE (ZIP): G2A 3S1

- (ii) TITLE OF INVENTION: SPECIES-SPECIFIC, GENIUS-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL AND FUNGAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES

- (iii) NUMBER OF SEQUENCES: 174

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

- (vi) PRIOR APPLICATION DATA:

(B) FILING DATE: 04-NOV-1996

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 1:

TGCTTTAGCA ACAGCCTATC AG

22

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TAAACTTCTT CCGGCACTTC G

21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGCGGCTATA AATGAAGAGG C

21

(2) INFORMATION FOR SEO ID NO: 4:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 4:

21

(2) INFORMATION FOR SEQ ID NO: 5:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

21

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

21

(2) INFORMATION FOR SEO ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGATCGAATT CCACATGAAG GTTATTATGA

30

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCTTCTCC CTCAACAATC AACTATCCT

30

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTTCACCAGC TGTATTAGAA GTA

23

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus agalactiae*

GTTCCCTGAA CATTATCTTT GAT

23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*

CAAGAAGGTT GGT TACAACC CAAAGA

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Candida albicans*

AGGTCTTACC AGTAACTTTA CCGGAT

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACTGACAAA CCATTCATGA TG

22

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AACTTCGTCA CCAACGCGAA C

21

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTGGCGCGGT ATGGTCGGTT

20

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GCCGACGTTG GAAGTGGTAA AG

22

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCGTGTTGAA CGTGGTCAAA TCAAA

25

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TRTGTGGTGT RATGWGCCA GGAGC

25

(2) INFORMATION FOR SEO ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACAACGTGGW CAAGTWTTAG CWGCT

25

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 20:

ACCATTTCWG TACCTTCTGG TAAGT

25

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

```
(A) NAME/KEY: misc_feature
(B) LOCATION:12
(D) OTHER INFORMATION:/note= "n = inosine"
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAAATTGCAG GNAAATTGAT TGA

23

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTACGCATGG CNTGACTCAT CAT

23

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:15
- (D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

2025-11-14 14:00:00

23

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "n = inosine"

(A) NAME/KEY: misc feature

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "n = inosine"

(A) NAME/KEY: misc feature

(B) LOCATION: 12

(D) OTHER INFORMATION: /note= "n = inosine"

(A) NAME/KEY: misc feature

(B) LOCATION: 18

(D) OTHER INFORMATION: /note= "n = inosine"

TNTCNC CNGGCATNAC CAT

23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TCGCTTCTCC

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 600 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(ii) MOLECULE TYPE: DNA (genomic)
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecium*
(xi) SEQUENCE DESCRIPTION: SEO ID NO: 26

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTCTTAGAGA | CATTGAATAT | GCCTTATGTC | GGCGCAGSCG | TATTGACCAG | TGCATGTGCC | 60 |
| ATGGATAAAA | TCATGACCAA | GTATATTTTA | CAAGCTGCTG | GTGTGCCGCA | AGTTCTTTAT | 120 |
| GTACCAGTAC | TTAAGAATCA | ATGGAAGAAG | AATCCTAAAA | AAGTATTTGA | TCAATGTGAA | 180 |
| GGTTCCTTGC | TTTATCCGAT | GTTTGTCAA | CCTGCGAATA | TGGGTTCTAG | TGTCGGCATT | 240 |
| ACAAAGGCAG | AAAACCGAGA | AGAGCTGCAG | AATGCTTTAG | CAACAGCCTA | TCAGTATGAT | 300 |
| TCTCGAGCAA | TCGTTGAACA | AGGAATTGAA | GCGCGCGAAA | TCGAAGTTGC | TGTATTAGGA | 360 |
| AATGAAGATG | TTCGGACGAC | TTTGCTTGCG | GAAGTCGTAA | AAGACGTAGC | ATTCTATGAT | 420 |
| TATGAAGCCA | AATATATCAA | TAATAAAATC | GAAATGCAGA | TTCCAGCCGA | AGTGC CGGAA | 480 |
| GAAGTTTATC | AAAAAGCGCA | AGAGTACGCG | AAGTTAGCTT | ACACGATGTT | AGGTGGAAGC | 540 |
| GGATTGAGCC | GGTGCATTTT | CTTTTGTACA | AATAAAAATG | AATTATTCCT | GAATGAATTA | 600 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GTGGGATTAA | ACAGATTTAT | GCGTGCGATG | ATGGTGGTTT | TCATTACTGC | CAATTGCAIT | 60 |
| ACGATTAAACC | CCGACATAAT | ATTTGACAGC | ACAGATAGCG | AAGATTCTAG | TCTAAACACA | 120 |
| GATGAATGGG | AAGAAGAAAA | AACAGAAGAG | CAACCAAGCG | AGGTAAATAC | GGGACCAAGA | 180 |
| TACGAAACTG | CACGTGAAGT | AAGTTACCGT | GATATTTAAG | AACTAGAAAA | ATCGAATAAA | 240 |
| GTGAGAAATA | CGAACAAAGC | AGACCTAATA | GCAATGTTGA | AAGAAAAAGC | AGAAAAAGGT | 300 |
| CCAAATATCA | ATAATAACAA | CAGTGAACAA | ACTGAGAATG | CGGCTATAAA | TGAAGAGGCT | 360 |

090904 11204

| | |
|---|------|
| TCAGGAGCCG ACCGACCAGC TATACAAGTG GAGCGTCGTC ATCCAGGATT GCCATCGGAT | 420 |
| AGCGCAGCGG AARTTAAAAA AAGAAGGAAA GCCATAGCAT CATCGGATAG TGAGCTTGAA | 480 |
| AGCCTTACTT ATCCGGATAA ACCAACAAAA GTAAATAAGA AAAAAGTGGC GAAAGAGTCA | 540 |
| GTTGCGGATG CTTCTGAAAG TGACTTAGAT TCTAGCATGC AGTCAGCAGA TGAGCTTCA | 600 |
| CCACAACCTT TAAAAGCAA CCAACAACCA TTTTCCCTA AAGTATTTAA AAAATAAAA | 660 |
| GATGCGGGGA AATGGGTACG TGATAAAATC GACGAAAATC CTGAAGTAAA GAAAGCGATT | 720 |
| GTTGATAAAA GTGCAAGGTT AATTGACCAA TTATTAACCA AAAAGAAAAG TGAAGAGGTA | 780 |
| AATGCTTCGG ACTTCCCGCC ACCACCTACG GATGAAGAGT TAAGACTTGC TTTGCCAGAG | 840 |
| ACACCAATGC TTCTTGTTTT TAATGCTCCT GCTACATCAG AACCGAGCTC ATTCGAATTT | 900 |
| CCACCACCAC CTACGGATGA AGAGTTAAGA CTTGCTTTGC CAGAGACGCC AATGCTTCTT | 960 |
| GGTTTAAATG CTCCTGCTAC ATCGGAACCG AGCTCGTTTCG AATTTCACC GCCTCCAACA | 1020 |
| GAAGATGAAC TAGAAATCAT CCGGGAACCA GCATCCTCGC TAGATTCTAG TTTTACAAGA | 1080 |
| GGGGAATTAG CTAGTTTGAG AAATGCTATT AATCGCCATA GTCAAAATTT CTCTGATTC | 1140 |
| CCACCAATCC CAACAGAAGA AGAGTTGAAC GGGAGAGGCG GTAGACCAAC ATCTGAAGAA | 1200 |
| TTTAGTTCGC TGAATAGTGG TGATTTTACA GATGACGAAA ACAGCGAGAC AACAGAAGAA | 1260 |
| GAAATTGATC GCCTAGCTGA TTTAAGAGAT AGAGGAACAG GAAAACACTC AAGAAATGCG | 1320 |
| GGTTTTTAC CATTAAATCC GTTTGCTAGC AGCCCGGTTTCTTCGTTAAG TCCAAAGGTA | 1380 |
| TCGAAAATAA GCGACCGGGC TCTGATAAGT GACATAACTA AAAAAACGCC ATTTAAGAAT | 1440 |
| CCATCACAGC CATTAAATGT GTTTAATAAA AAAACTACAA CGAAAACAGT GACTAAAAAA | 1500 |
| CCAACCCCTG TAAAGACCGC ACCAAAGCTA GCAGAACTTC CTGCCACAAA ACCACAAGAA | 1560 |
| ACCGTACTTA GGGAAAATAA AACACCCCTT ATAGAAAAAC AAGCAGAAAC AAACAAGCAG | 1620 |
| TCAATTAATA TGCCGAGCCT ACCAGTAATC CAAAAAGAAG CTACAGAGAG CGATAAAGAG | 1680 |
| GAAATGAAC CACAAACCGA GGAAAAAATG GTAGAGGAAA GCGAATCAGC TAATAACGCA | 1740 |
| AACGAAAAAT ATCGTTCTGC TGGCAITGAA GAAGGAAAC TAATTGCTAA AAGTGCAGAA | 1800 |
| GACGAAAAAG CGAAGGAAGA ACCAGGGAAC CATACGACGT TAATTCTTGC AATGTTAGCT | 1860 |
| ATTGCGCTGT TCTCTTTAGG GCGCTTTATC AAAATTATTC AATTAAGAAA AAATAATTAA | 1920 |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TACCGGTACG | CTAAATATTG | GTGATGTATT | GGATATTATG | ATTTGGGAAG | CGCCGCCAGC | 60 |
| GGTATTGTIT | GGTGTGGCC | TTTCTTCGAT | GGGCTCGGGT | AGTGCGCAAC | AAACCAAGTT | 120 |
| GCCGGAGCAA | CTGGTGACGG | CACGTGGTAC | GGTTTCTGTG | CCGTTTGTTG | GCGATATTTC | 180 |
| GGTGGTCGGT | AAACGCCTTG | GTCAGGTTCA | GGAAATTATT | AAAGGCCGCC | TGAAAAAAT | 240 |
| GGCCAATCAG | CGCAAGTGA | TGGTGCCTT | GGTGCAGAA | AATGCGCCAA | ATGTATCGGT | 300 |
| GATTTCGCGA | GGCAATAGTG | TGCGTATGCC | GTTGACGGCA | GCCGGTGAGC | GTGTGTTGGA | 360 |
| TGCGGTGGCT | GCGGTAGGTG | GTTCAACGGC | AAATGTGCAG | GATACGAATG | TGCAG | 415 |

(2) INFORMATION FOR SEO ID NO: 29:

(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| TCGCTTCTCC | AGAAGAAATT | TTAGAAACAT | ATCTAGAAAA | TCCCAAATTA | GATAAACCGT | 60 |
| TTATATTATG | TGAATACGCA | CATGCAATGG | GAAAATTCACC | AGGAGATCTT | AATGCATATC | 120 |
| AAACATTAAT | TGAAAAATAT | GATAGTTTTA | TTGGCGGTTT | TGTTTGGGAA | TG GTGTGATC | 180 |
| ATAGCATTCA | GGTTGGGATA | AAGGAAGGTA | AACCAATTTT | TAGATATGGT | GGAGATTTTG | 240 |
| GTGAGGCCTT | ACATGACGGT | AATTTTTGTG | TTGATGGTAT | TGTTTCGCCA | GATCGAATTC | 300 |
| CACATGAAGG | TTATTATGAG | TTTAAACATG | AACATAGACC | TTTGAGATTG | GTTAACGAAG | 360 |
| AGGATTATCG | GTTTACATTG | AAGAATCAAT | TTGATTTTAC | AAATGCGGAG | GATAGTTTGA | 420 |
| TTGTTGAGGG | AGAAGCGA | | | | | 438 |

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

| | |
|--|-----|
| ATGAACGTTA CACATATGAT GTATCTATCT GGAACCTAG TGGCTGGTGC ATTGTTATTT | 60 |
| TCACCAGCTG TATTAGAAGT ACATGCTGAT CAAGTGACAA CTCACAAAGT GGTAAATCAT | 120 |
| GTAAATAGTA ATAATCAAGC CCAGCAAATG GCTCAAAGC TTGATCAAGA TAGCATTACAG | 180 |
| TTGAGAAATA TCAAAGATAA TGTTCAGGGA ACAGATTATG AAAAACCGGT TAATGAGGCT | 240 |
| ATTACTAGCG TGGAAAAATT AAAGACTTCA TTGCGTGCCA ACCCTGAGAC AGTTTATGAT | 300 |
| TTGAATTCTA TTGGTAGTCG TGTTAGAAGCC TTAACAGATG TGATTGAAGC AATCATTTTT | 360 |
| TCAACTCAAC ATTTAACAAA TAAGGTTAGT CAAGCAAATA TTGATATGGG ATTTGGGATA | 420 |
| ACTAAGCTAG TTATTCGCAT TTTAGATCCA TTTGCTTCAG TTGATTCAAT TAAAGCTCAA | 480 |
| GTTAACGATG TAAAGGCATT AGAACAAAAA GTTTTAACTT ATCCTGATTT AAAACCAACT | 540 |
| GATAGAGCTA CCATCTATAC AAAATCAAAA CTTGATAAGG AAATCTGGAA TACACGCTTT | 600 |
| ACTAGAGATA AAAAAGTACT TAACGTCAAA GAATTTAAAG TTTCAARTAC TTTAAATAAA | 660 |
| GCAATCACAC ATGCTGTTGG AGTTTCAGTTG AATCCAAATG TTACGTTACA ACAAGTTGAT | 720 |
| CAAGAGATTG TAACATTACA AGCAGCACTT CAAACAGCAT TAAAATAA | 768 |

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

030304-11201

(2) INFORMATION FOR SEO ID NO: 32:

- | | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| TTCATAGACG | CTGAGCAGCG | TTTGGATCCA | TCTTACGCGG | CTGCTCTAGG | TGTAATAAT | 60 |
| GATGAGCTGT | TGCTATCTCA | ACCAGATTCT | GGTGAGCAAG | GTTTAGAAAT | TGCAGGAAAA | 120 |
| TTGATTGACT | CTGGGGCAGT | TGATTTAGTT | GTTCATCGACT | CTGTTGCAGC | TCTTGTACCA | 180 |
| CGTGCGGAAA | TCGATGGAGA | TATCGGTGAT | AGC | | | 213 |

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 692 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Streptococcus mutans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33
```

GGGCCGGAAT CTTCTGGTAA GACAAC TGTC GCTCTTCATG CTGCTGCTCA GGCGCAAAAA 60

| | |
|---|-----|
| GATGGCGGTA TTGCCGCTTT CATTGATGCA GAACATGCCC TTGATCCAGC CTATGCTGCT | 120 |
| GCTCTTGGCG TTAATATTGA TGAGCTTTTG CTTTCAACA CAGATTCAGG AGAACAGGGT | 180 |
| CTTGAAATTG CAGGGAAATT GATTGATTCT GCGCTGTGT ATTTAGTTGT TGTTGACTCA | 240 |
| GTGGCAGCTT TAGTACCACG TCGCGAGATT GACGGAGATA TTGGTAATAG TCATGTTGGC | 300 |
| TTACAAGCAC GCATGATGAG TCAAGCGATG CGTAAATTAT CAGCTTCAAT CAATAAACA | 360 |
| AAAACCATG CTATTTTAT TAATCAATTG CGGGAAAAAG TTGGTATTAT GTTTGGTAAT | 420 |
| CCAGAAACAA CCCCTGGCGG GCGTGCTTG AAGTTTTATT CTCTGTGCG TCTTGATGTC | 480 |
| CGCGGCAATA CTCAAATTAA AGGAACCGGG GAACAAAAAG ACAGCAATAT TGGTAAAGAG | 540 |
| ACCAAAATTA AAGTTGTTAA AAATAAAGTT GCTCCACCAT TTAAGGAAGC TTTTGTAGAA | 600 |
| ATTATATATG GTGAAGGCAT TTCTCGTACA GGTGAATTAG TTAAGATTGC CAGTGATTG | 660 |
| GGAATTATCC AAAAAGCTGG AGCTTGTAC TC | 692 |

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

| | |
|---|-----|
| ATGGCGAAAA AACCAAAAA ATTAGAAGAA ATTTCAAAAA AATTGGGGC AGAACGTGAA | 60 |
| AAGCCTTGA ATGACGCTCT TAAATTGATT GAGAAAGACT TTGGTAAAGG ATCAATCATG | 120 |
| CGTTTGGGTG AACGTGCGGA GCAAAGGTG CAAGTGATGA GCTCAGGTTT TTAGCTCTT | 180 |
| GACATTGCCC TTGGCTCAGG TGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCA | 240 |
| GAGTCATCTG GTAAGACAAC GGTGCCCCCT CATGCAGTTG CACAAGCGCA AAAAGAAGGT | 300 |
| GGGATTGCTG CCTTTATCGA TCGGGAACAT GCCCTTGATC CAGCTTATGC TCGGGCCCTT | 360 |
| GGTGTCAATA TTGACGAATT GCTCTTGCTC CAACCAGACT CAGGAGAGCA AGGCTTGAG | 420 |
| ATTGCGGGAA AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT | 480 |
| GCCCTTGTTT CTCGTGCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGCAG | 540 |
| GCTCGTATGA TGAGCCAGGC CATGCGTAAA CTTGGCGCCT CTATCAATAA AACCAAAACA | 600 |

0909043.112001

(2) INFORMATION FOR SEO ID NO: 35:

(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| ATGCGTCTCAG | GAAGTCTAGC | TCTTGATATT | GCTTGGATAG | CTGTGGTTA | TCCTAAAGGA | 60 |
| CGTATCATCG | AAATCTATGG | TCCAGAGTCT | TCCGGTAAAA | CGACTGTGGC | TTTACATGCT | 120 |
| GTAGCACAAG | CTCAAAAAGA | AGGTGGAATC | GCAGCCTTTA | TCGATGCCGA | GCATGCGCTT | 180 |
| GATCCAGCTT | ATGCTGCTGC | GCTTGGGGTT | AATATTGATG | AACCTCTCTT | GTCTCAACCA | 240 |
| GATTCGTGAG | AACAAGGACT | TGAAATTGCA | GGTAAATTGA | TTGATTCTGG | TGCGGTTGAC | 300 |
| CTGGTGTGTT | TCGATTCACT | AGCAGCTTTA | GTGCCACGTG | CTGAAATTGA | TGGTGATATT | 360 |
| GGCGATAGCC | ATGTCGAGAT | GCAAGCAGCT | ATGATGAGTC | AGGCCATGCG | TAAATTATCA | 420 |
| GCTTCTATTA | ATAAAACAAA | AACTATCGCA | ATCTTTATCA | ACCAATTGCG | TGAAAAAGTT | 480 |
| GGTGTGATGT | TTGGAATACC | TGAAACAACA | CCAGTGGTTC | GAGCTTTGAA | ATTCTATGCT | 540 |
| TCTGTTCCGC | TGGATGTGCG | TGGAACAAC | CAAAATAAAG | GAACTGGTGA | CCAAAAGATA | 600 |

(2) INFORMATION FOR SEQ ID NO: 36:

- | | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|-----|
| CGCATATGCAC | GAGCTCTAGG | TGTTAATATC | GATGAGCTTC | TTTTGTGCGCA | GCCTGATTCT | 60 |
| GGTGAGCAAG | GTCTCGAAAT | TGCAGGTAAG | CTGATTGACT | CTGTGTGCACT | GGATTTAGTT | 120 |
| GTGTGTTGACT | CAGTTGCGGC | CTTCGTACCA | CGTGCAGAAA | TTGATGGAGA | TAGTGGTGAC | 180 |
| AGTCATGTAG | GACTTCAAGC | CGCATATGATG | AGTCAAGCCA | TGCGTAAACT | TTCGCATCT | 240 |
| ATTAATAAAA | CAAAAACGAT | TGCTATCTTT | ATTAAACAGT | TGCGTGAAAA | AGTTGGTATC | 300 |
| ATGTTTGGA | AC | | | | | 312 |

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

(2) INFORMATION FOR SEO ID NO: 38:

(ii) MOLECULE TYPE: DNA (genomic)

CGCAGTGTTA TCACTCATGG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGAATGAAG CCATACCAA

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

ATCAGCAATA AACCCAGCCAG

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TTACCATGAG CGATAACAGC

20

(2) INFORMATION FOR SEQ ID NO: 42:

(ii) MOLECULE TYPE: DNA (genomic)

CTCATT CAGT TCCGTTTCCC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CAGCTGCTGC AGTGGATGGT

20

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CGCTCTGCTT TGTTATTCGG

20

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TACGCCAACA TCGTGGAAAG

20

(2) INFORMATION FOR SEQ ID NO: 46:

(ii) MOLECULE TYPE: DNA (genomic)

TTGAATTGG CTTCTTCGGT

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGGATACAGA AACGGGACAT

20

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TAAATCTTTT TCAGGCAGCG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGGTTTGA AGGGTTTATT ATAAG

25

(2) INFORMATION FOR SEQ ID NO: 50:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

25

(2) INFORMATION FOR SEQ ID NO: 51:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

21

(2) INFORMATION FOR SEQ ID NO: 52:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

21

(2) INFORMATION FOR SEO ID NO: 53:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

20

(2) INFORMATION FOR SEO ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CAGCTGTTAC AACGGACTGG

20

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCTATGATCT CGCAGTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATCGTCACCG TAATCTGCTT

20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CAATTCTCGAT TGCTTTGCTA

20

(2) INFORMATION FOR SEQ ID NO: 58:

00000000-112001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CGAAATGCT TCTCAAGATA

20

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CTGGATTATG GCTACGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AGCAGTGTGA TGGTATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACTCTTGAT GAAGTGTCTGG

20

(2) INFORMATION FOR SEQ ID NO: 62:

090904 1001

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

20

(2) INFORMATION FOR SEQ ID NO: 63:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

20

(2) INFORMATION FOR SEQ ID NO: 64:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

20

(2) INFORMATION FOR SEQ ID NO: 65:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

20

(2) INFORMATION FOR SEQ ID NO: 66:

(ii) MOLECULE TYPE: DNA (genomic)

GTGTTTGAAC CATGTACACG

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGTAGAGGTC TAGCCCGTGT

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

ACGGGGATAA CGACTGTATG

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ATAAAGATGA TAGGCCGGTG

20

(2) INFORMATION FOR SEQ ID NO: 70:

(ii) MOLECULE TYPE: DNA (genomic)

TGCTGTCATA TTGTCTTGCC

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATTATCTTCG GCGGTTGCTC

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACTATCGGC TTCCCATTC

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGATAGAAGC AGCAGGACAA

20

(2) INFORMATION FOR SEQ ID NO: 74:

(ii) MOLECULE TYPE: DNA (genomic)

CTGATGGATG CGGAAGATAC

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GCCTTATGTA TGAACAAATG G

21

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GTGACTTTWG TGATCCCTTT TGA

23

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

TCCAATCATT GCACAAAATC

20

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AATTCCCTCT ATTTGGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCCCAAGCCA GTAAAGCTAA

20

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TGGTTTTTCA ACTTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

TCATAGAATG GATGGCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 82:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

22

(2) INFORMATION FOR SEQ ID NO: 86:

(ii) MOLECULE TYPE: DNA (genomic)

CCTTTACTCC AATAATTGG CT

22

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TTTCATCTAT TCAGGATGGG

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGAGCAACAT TCTTTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TGTGCCTGAA GAAGGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CGTGTACTT CACCACCACT

20

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TATCTTATCG TTGAGAAGGG ATT

23

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTACACTTGG CTTAGGATGA AA

22

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CTATCTGATT GTTGAAGAAG GATT

24

(2) INFORMATION FOR SEQ ID NO: 94:

0993643.112001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GTCTACTCTT GGTTTAGGAT GAAA

24

- (2) INFORMATION FOR SEQ ID NO: 95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CTGTGTGATC ACGATAATTT CC

22

- (2) INFORMATION FOR SEQ ID NO: 96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

ATCTTTTAGC AAACCCGTAT TC

22

- (2) INFORMATION FOR SEQ ID NO: 97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AACAGGTGAA TTATTAGCAC TTGTAAG

27

- (2) INFORMATION FOR SEQ ID NO: 98:

0308043-12001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATTGCTGTTA ATATTTTTTG AGTTGAA

27

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GTGATCGAAA TCCAGATCC

19

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

ATCCTCGGTT TTCTGGAAG

19

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CTGGTCATAC ATGTGATGG

19

(2) INFORMATION FOR SEQ ID NO: 102:

09995-3 1201

(ii) MOLECULE TYPE: DNA (genomic)

GATGTTACCC GAGAGCTTG

19

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTAAGCGTGC ATAATAAGCC

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

TTGCGATTAC TTCGCCAACT

20

(2) INFORMATION FOR SEO ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTTACTAAGC TTGCCCCCTTC

20

(2) INFORMATION FOR SEO ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAAGGCAGC AATTATGAGC

20

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:9
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:12
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:15
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:18
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:21
 - (D) OTHER INFORMATION:/note= "n = inosine"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AAYATGATNA CNGGNGCNGC NCARATGGA

29

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid

100211-4160660

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 3

(D) OTHER INFORMATION:/note= "n = inosine"

(ix) **FEATURE:**

(A) NAME/KEY: misc feature

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION:12

(D) OTHER INFORMATION:/note= "n = inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCNACNGTNC KNCCRCCTTC RCG

23

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION: 12

(D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION:15

(D) OTHER INFORMATION: /note= "n = inosine"

(ix) FEATURE:

(A) NAME/KEY: misc feature

(D) OTHER INFORMATION: /note= "n = inosine"

CARYTNATHG TNGCNGTNAA YAARATGGA

29

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(D) FORECAST: INFLATE

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATGAAAAACA CAATACATAT CAACTTCGCT ATTTTITTTAA TAATTGCAA TATTATCTAC 60

AGCAGCGCCA GTGCATCAAC AGATATCTCT ACTGTTGCAT CTCCATTATT TGAAGGAACT 120

GAAGGTTGTT TTTTACTTTA CGATGCATCC ACAAACGCTG AAATTGCTCA ATTCAATAAA 180

GCAGAGTGTG CAACGCAAAAT GGCACCAGAT TCAACTTTCA AGATCGCATT ATCACTTATG 240

GCATTGATG CGGAAATAAT AGATCAGAAA ACCATATTCA AATGGGATAA AACCCCCAAA 300

GGAATGGAGA TCTGGAACAG CAATCATACA CCAAAGACGT GGATGCAATT TTCTGTTGTT 360

TGGGTTTCGC AAGAAATAAC CCAAAAAATT AGATTAAATA AAATCAAGAA TTATCTCAA 420

GATTTTGATT ATGGAAATCA AGACTTCTCT GGAGATAAAG AAAGAAACAA CGGATTAACA 480

GAAGCATGGC TCGAAAGTAG CTTAAAAATT TCACCAGAAG AACAAATTCA ATTCCTGCGT 540

AAAATTATTA ATCACAATCT CCCAGTTAAA AACTCAGCCA TAGAAAACAC CATAGAGAAC 600

ATGTATCTAC AAGATCTGGA TAATAGTACA AAACCTGTATG GGAAAACTGG TGCAGGATTC 660

ACAGCAATA GAACCTTACA AACCGGATGG TTTGAAGGGT TTATTATAAG CAAATCAGGA 720

CATAAATATG TTTTGTGTC CGCACTTACA GGAAACTTGG GGTCGAATTT AACATCAAGC 780

ATAAAAGCCA AGAAAAATGC GATCACCATT CTAAACACAC TAAATTTATA A 831

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

| | |
|---|-----|
| TTGAAAAAGT TAATATTTTT AATTGTAATT GCTTTAGTTT TAAGTGCATG TAATTCAAAC | 60 |
| AGTTCACATG CCAAAGAGTT AAATGATTTA GAAAAAAAT ATAATGCTCA TATTGGTGT | 120 |
| TATGCTTTAG ATACTAAAG TGGTAAGGAA GTAAAATTTA ATTCAAGATA GAGATTGCC | 180 |
| TATGCTTCAA CTTCAAAAGC GATAAATAGT GCTATTTTGT TAGAACAAGT ACCTTATAAT | 240 |
| AAGTTAAATA AAAAAGTACA TATTAACAAA GATGATATAG TTGCTTATTC TCCTATTTTA | 300 |
| GAAAAATATG TAGGAAAAGA TATCACTTTA AAAGCACTTA TTGAGGCTTC AATGACATAT | 360 |
| AGTGATAATA CAGCAACAA TAAAATTATA AAAGAAATCG GTGGAATCAA AAAAGTTAAA | 420 |
| CAACGTCTAA AAGAACTAGG AGATAAAGTA ACAAATCCAG TTAGATATGA GATAGAATTA | 480 |
| AATTACTATT CACCAAGAG CAAAAAGAT ACTTCAACAC CTGCTGCTTT CGGTAAGACT | 540 |
| TTAAATAAAC TTATCGCAA TGGAAAATTA AGCAAAGAAA ACRAAAATTT CTTACTTGAT | 600 |
| TTAATTGTAA ATAATAAAG CGGAGATACT TTAATTAAAG ACGGTGTTCC AAAAGACTAT | 660 |
| AAGGTGCTG ATAAAAGTG TCAAGCAATA ACATATGCTT CTAGAAATGA TGTGCTTTT | 720 |
| GTTTATCCTA AGGGCCAATC TGAACCTATT GTTTTAGTCA TTTTACGAA TAAAGACAAT | 780 |
| AAAAGTGATA AGCCAAATGA TAAGTTGATA AGTGAAACCG CCAAGAGTGT AATGAAGGAA | 840 |
| TTTTAA | 846 |

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

| | |
|---|-----|
| ATGTCCGCGA GCACCCCCC CATAACTCTT CGCCTCATGA CCGAGCGCGA CCTGCCGATG | 60 |
| CTCCATGACT GGCTCAACCG GCCGCACATC GTTGAGTGGT GGGGTGCGCA CGAAGAGCGA | 120 |
| CCGACTCTTG ATGAAGTGCT GGAACACTAC CTGCCAGAG CGATGGCGGA AGAGTCCGTA | 180 |
| ACACCGTACA TCGAATGCT GGGCGAGGAA CCGATCGGCT ATGCTCAGTC GTACGTCGCG | 240 |
| CTCGGAAGCG GTGATGGCTG GTGGGAAGAT GAAACTGATC CAGGAGTGCG AGGAATAGAC | 300 |
| CAGTCTCTGG CTGACCCGAC ACAGTTGAAC AAAGGCCTAG GAACAAGGCT TGTCCGCGCT | 360 |

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(2) INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

(2) INFORMATION FOR SEQ ID NO: 114:

(A) LENGTH: 738 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

| | |
|--|-----|
| ATGAACAAAA ATATAAAATA TTCTCAAAAC TTTTAAACGA GTGAAAAAGT ACTCAACCAA | 60 |
| ATAATAAAAC AATTGAATTT AAAAGAAACC GATACCGTTT ACGAAATTGG AACAGGTAAA | 120 |
| GGGCATTTAA CGACGAAACT GGCCTAAAATA AGTAAACAGG TAACGTCTAT TGAATTAGAC | 180 |
| AGTCATCTAT TCACTTATC GTCAGAAAAA TTAATTCGA ATACTCGTGT CACTTTAATT | 240 |
| CACCAAGATA TTCTACAGTT TCAATTCCCT AACAAACAGA GGTATAAAAT TGTTGGGAAT | 300 |
| ATTCCTTACC ATTTAAGCAC ACAAATTATT AAAAAAGTGG TTTTGAAG CCATGCGTCT | 360 |
| GACATCTATC TGATTGTTGA AGAAGGATTC TACAAGCGTA CCTTGGATAT TCACCGAACA | 420 |
| CTAGGGTTGC TCTTGCACAC TCAAGTCTCG ATTCAGCAAT TGCTTAAGCT GCCAGCGGAA | 480 |
| TGCTTTCATC CTAAACCAAG AGTAAACAGT GTCTTAATAA AACTTACCG CCATACCACA | 540 |
| GATGTTCCAG ATAAATATTG GAAGCTATAT ACGTACTTTG TTTCAAAATG GGTCAATCGA | 600 |
| GAATATCGTC AACTGTTTAC TAAAAATCAG TTTCATCAAG CAATGAAACA CGCCAAAGTA | 660 |
| AACAATTAA GTACCGTTAC TTATGAGCAA GTATTGTCTA TTTTAAATAG TTATCTATTA | 720 |
| TTTAACGGGA GGAATAA | 738 |

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

| | |
|---|-----|
| ATGAACGAGA AAAATATAAA ACACAGTCAA AACTTTATTA CTTCAAAACA TAATATAGAT | 60 |
| AAAATAATGA CAAATATAAG ATTAATGAA CATGATAATA TCTTTGAAAT CGGCTCAGGA | 120 |
| AAAGGGCATT TTACCCTTGA ATTAGTACAG AGGTGTAATT TCGTAAGTGC CATTGAAATA | 180 |
| GACCATAAAT TATGCAAAAC TACGAAAAAT AAAGTTGTTG ATCAGATAAA TTCCAAGTT | 240 |
| TTAAACAAGG ATATATTGCA GTTTAAATTT CCTAAAAACC AATCCTATAA AATATTGGGT | 300 |
| AATATACCTT ATAACATAAG TACGGATATA ATACGCAAAA TTGTTTTTGA TAGTATAGCT | 360 |
| GATGAGATTT ATTTAATCGT GGAATACGGG TTTGCTAAAA GATTATTAAA TACAAAACGC | 420 |
| TCATTGGCAT TATTTTTAAT GGCAGAAGTT GATATTTCTA TATTAAGTAT GGTTCGAAGA | 480 |

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| | |
|---|-----|
| GAATATTTTC ATCCTAAACC TAGAGTGAAT AGCTCACTTA TCAGATTAAA TAGAAAAAAA | 540 |
| TCAAGAATAT CACACAAAGA TAAACAGAAG TATAATTATT TCGTTATGAA ATGGGTTAAC | 600 |
| AAAGAATACA AGAAAATATT TACAAAAAAT CAATTTAACA ATTCCTTAAA ACATGCAGGA | 660 |
| ATTGACGATT TAAACAATAT TAGCTTTGAA CAATTCTTAT CTCTTTTCAA TAGCTATAAA | 720 |
| TTATTTAATA AGTAA | 735 |

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1029 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

| | |
|--|------|
| ATGAATAAAA TAAAAGTCGC AATTATCTTC GCGCGTTGCT CGGAGGAACA TGATGTGTCG | 60 |
| GTAAAATCCG CAATAGAAAT TGCTGCGAAC ATTAATACTG AAAAATTCGA TCCGCACTAC | 120 |
| ATCGGAATTA CAAAAACGG CGTATGGAAG CTATGCAAGA AGCATGTAC GGAATGGGAA | 180 |
| GCCGATAGTC TCCCCGCCAT ATTCGCCCG GATAGGAAAA CGCATGGTCT GCTTGTCTATG | 240 |
| AAAGAAAGAG AATACGAAAC TCGGCGTATT GACGTGGCTT TCCCGGTTTT GCATGGCAAA | 300 |
| TGCGGGGAGG ATGGTGCGAT ACAGGGTCTG TTTGAATTGT CTGGTATCCC CTATGTAGGC | 360 |
| TGCGATATTC AAAGCTCCGC AGCTTGCAATG GACAAATCAC TGGCCTACAT TCTTACAAAA | 420 |
| AATGCGGGCA TCGCCGTCCT CGAATTTCAA ATGATTGAAA AAGGTGACAA ACCGGAGGCG | 480 |
| AGGACGCTTA CCTACCTGT CTTTGTAAG CCGGCACGGT CAGGTTCGTC CTTTGGCGTA | 540 |
| ACCAAAGTAA ACAGTACGGA AGAACTAAAC GCTCGCATAG AAGCAGCAGG ACAATATGAT | 600 |
| GGAAAAATCT TAATTGAGCA AGCGATTTCG GGCTGTGAGG TCGGCTGCGC GGTATGCGGA | 660 |
| AACGAGGATG ATTTGATTGT CGGCGAAGTG GATCAAATCC GGTGTAGCCA CGGTATCTTC | 720 |
| CGCATCCATC AGGAAAACGA GCCCGAAAAA GGCTCAGAGA ATGCGATGAT TATCGTTCCA | 780 |
| GCAGACATTC CGGTGAGGA ACGAAATCGG GTGCAAGAAA CGGCAAGAAA AGTATATCGG | 840 |
| GTGCTTGATG GCAGAGGGCT TGCTCGTGTT GATCTTTTTT TGCAAGGAGA TGGCGGCATC | 900 |
| GTTCTAAACG AGGTCAATAC CCTGCCCGGT TTTACATCGT ACAGCCGCTA TCCACGCATG | 960 |
| GCGGCTGCCG CAGGAATCAC GCTTCCCGCA CTAATTGACA GCCTGATTAC ATTGGCGATA | 1020 |

09989471201

GAGAGGTGA

1029

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1031 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

| | |
|--|------|
| ATGAAAAAAA TTGCCGTTTT ATTTGGAGGG AAMTCTCCAG AATACTCAGT GTCAC TAACC | 60 |
| TCAGCAGCAA GTGTGATCCA AGCTATTGAC CCGCTGAAAT ATGAAGTAAT GACCATTGGC | 120 |
| ATCGCACCAA CAATGGATTG GTATTGGTAT CAAGGAAACC TCGCGAATGT TCGCAATGAT | 180 |
| ACTTGGCTAG AAGATCACA AAACGTGCAC CAGCTGACIT TTTCTAGCCA AGGATTTATA | 240 |
| TTAGGAGAAA AACGAATCGT CCCTGATGTC CTCTTTCCAG TCTTGCAATG GAAGTATGGC | 300 |
| GAGGATGGCT GTATCCAAGG ACTGCTTGAA CTAATGAACC TGCCCTTATGT TGGTTGCCAT | 360 |
| GTCGCTGCCT CCGCATTATG TATGAACAAA TGGCTCTTGC ATCAACTTGC TGATACCATG | 420 |
| GGAATCGCTA GTGCTCCAC TTTGCTTTTA TCCGCTATG AAAACGATCC TGCCACAATC | 480 |
| GATCGTTTTA TTCAAGACCA TGGATTCCCG ATCTTTATCA AGCCGAATGA AGCCGGTTCT | 540 |
| TCAAAAGGGA TCACAAAAGT AACTGACAAA ACAGCGCTCC AATCTGCATT AACGACTGCT | 600 |
| TTTGCTTACG GTTCTACTGT GTTGATCCAA AAGGCGATAG CGGGTATTGA AATTGGCTGC | 660 |
| GGCATCTTAG GAAATGAGCA ATTGACGATT GGTGCTTGTG ATGCGATTTT TCTTGTGAC | 720 |
| GGTTTTTTTG ATTTTGAAGA GAAATACCAA TTAATCAGCG CCAAGCATCAG TGTCACGACA | 780 |
| CCATTGCCTC TCGCGCTTGA ATCAGATC AAGGAGCAGG CACAGCTGCT TTATCGAAAC | 840 |
| TTGGGATTGA CGGGTCTGGC TCGAATCGAT TTTTTCGTCA CCAATCAAGG AGCGATTTAT | 900 |
| TTAAACGAAA TCAACACCAT GCCGGGATTT ACTGGGCACT CCCGCTACCC AGCTATGATG | 960 |
| GCGGAAGTCG GGTATACCTA CGAAATATTA GTAGAGCAAT TGATTGCACT GGCAGAGGAG | 1020 |
| GACAAACGAT G | 1031 |

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 809 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia adiacens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

| | |
|---|-----|
| TGGTGCTATC TTAGTAGTAT CTGCAGCTGA TGGTCCAATG CCTCAAACAC GTGAACACAT | 60 |
| CTTATTATCA CGTCAAGTAG GTGTTCTTCA CATCGTTGTA TTCTTAAACA AAGTTGACAT | 120 |
| GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTATCAGA | 180 |
| ATACGATTTC CCAGGCGATG ACACTCCAGT TGTTCAGGT TCTGCTTTAC GCGCTTTAGA | 240 |
| AGGCGAGCCT TCATACRAAG AAAAAATCTT AGAATTATG GCTGCTGTTG ACGAATACAT | 300 |
| TCCAACTCCA GAACGYGACG TTGACAAACC ATTCATGATG CCAGTTGAAG ACGTGTCTTC | 360 |
| AATCACAGGT CGTGGTACTG TTGCTACAGG TCGTGTGTA GCGTGACRAG TTCGTGTTGG | 420 |
| TGACGAAGTT GAAATCGTTG GTATTTTCAGA AGAAACTTCA AAAACAACCTG TAACTGGTGT | 480 |
| TGAAATGTTC CGTAAATTGT TAGACTACGC TGAAGCAGGG GATAACATTG GTACATTATT | 540 |
| ACGTGGTGTT ACACGTGACA ACATCGAACG TGGACAAGTT CTGCTAAAC CAGGAACAAT | 600 |
| CACTCCACAT ACTAAATICA AAGCTGAAGT TTACGTATTA ACTAAAGAAG AAGGTGGACG | 660 |
| TCATACTCCA TTCTTCTCTA ACTACCGTCC TCAATTCTAC TTCCGTACAA CAGACATCAC | 720 |
| TGGTGTTTGT GTGTTACCA GAGGCGTTGA AATGGTAATG CCTGGTGATA ACGTAACAT | 780 |
| GGAAGTTGAA TTAATTCACC CAGTAGCGA | 809 |

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Abiotrophia defectiva*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

| | |
|---|-----|
| CGGCGCGATC CTCGTGTGAT CTGCTGCTGA CGGCCCAATG CCACAAACTC GTGAACACAT | 60 |
| CCTCTGTGCT CGTCAAGTTG GTGTTCTTCA CATCGTAGTA TTCTTGAACA AAGTTGACAT | 120 |

(2) INFORMATION FOR SEQ ID NO: 120:

(A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|-----|
| CTCTGTCAAA | TGGGACAAAA | ACAGATTGTA | AGAAATCATC | AAGGAAACCT | CCAACTTCGT | 60 |
| CAAGAAGGTT | GTTTACAACC | CAAAGACTGT | TCCATTCGTT | CCAATCTCTG | GTTGGAATGG | 120 |
| TGACAACWTG | ATTGAASCAT | CCACCAACTG | TCCATTGTTAC | AAGGGTTGGG | AAAAGGAAAC | 180 |
| CAAATCCGGT | AAAGTTACTG | GTAAGACCTT | GTTAGAAGCT | ATTGACGCTA | TTGAACCACC | 240 |
| AACCAGACCA | ACCGACAAAC | CATTGAGATT | GCCATTTRCAA | GATGTTTACA | AGATCGGTGG | 300 |
| TATTGGTACT | GTGCCAGTCTG | GTAGAGTTGA | AACTGGTATC | ATCAAAGCCG | GTATGGTWTG | 360 |
| TACTTTTCGCC | CCAGCTGGTG | TTACCACTGA | AGTCAARTCC | GTTGAAATGC | ATCACGAACA | 420 |
| ATTGGCTGAA | GGTGTTCCAG | GTGACAATGT | TRGTTTCAAC | GTTAAGAAAC | TTTCCGTTAA | 480 |
| AGAAATTAGA | AGAGGTAACG | TTTGTGGTGA | CTCCAAGAAC | GATCCACCAA | AGGGTTGTGA | 540 |

(2) INFORMATION FOR SEQ ID NO: 121:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TCTGTCAAGT | GGGATGAATC | CAGATTTCGT | GAAATCGTTA | AGGAAACCTC | CAACTTCATC | 60 |
| AAGAAGGTCG | GTTACAACCC | AAAGACTGTT | CCATTCTGTC | CAATCTCTGG | TTGGAACGGT | 120 |
| GACAAACATGA | TTGAAGCCAC | CACCAACGCT | TCCTGGTACA | AGGGTTGGGA | AAAGGAAACC | 180 |
| AAGGCTGTGGT | TCGTCAAGGG | TAAGACCTTG | TTGGAAGCCA | TTGACGCTAT | CGAACCACCA | 240 |
| ACCAGACCAA | CTGACAAGCC | ATTGAGATTG | CCATTGCAAG | ATGTCTACAA | GATCGGTGGT | 300 |
| ATCGGTACGG | TGCCAGTCGG | TAGAGTCGAA | ACCGGTGTCA | TCAAGCCAGS | TATGGTTGTT | 360 |
| ACCTTCGCCC | CAGCTGSGTG | TACCACTGAA | GTCAAGTCCG | TTGAATGCA | CCACGAACAA | 420 |
| TTGACTGAAG | GTTTGCCAGG | TGACAACGTT | GGTTTCAACG | TTAAGAACGT | TTCCGTTAAG | 480 |
| GAAATCAGAA | GAGGTAATGT | CTGTGGTGAC | TCCAAGAACG | ACCCACCAAA | GGCTGTGCT | 540 |
| TCTTTCACAG | CTACCGTCAT | TGTCTTGAAC | CACCCAGGTC | AAATCTCTGC | TGGTTACTCT | 600 |
| CCAGTTTTTG | ACTGTACAC | CGCCCACATT | GCTTGTAAAT | TCGAAGAATT | GTTGGAAAAG | 660 |
| AACGACAGAA | GATCCGGTAA | GAAGTTGGAA | GACTCTCCAA | AGTTCTTGAA | GTCGGGTGAC | 720 |
| GCTGCTTTGG | TTAAGTTCGT | TCCATCCAAG | CCA | | | 753 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida krusei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

| | |
|---|-----|
| CCGTTAAGTG GGATGAAAAC AGATTGAAG AATTGTCAA GGAAACCCAA AACTTCATCA | 60 |
| AGAAGGTTGG TTACAACCCA AAGACTGTTT CATTCTGTC AATCTCTGGT TGGAATGGTG | 120 |
| ACAACATGAT TGAAGCATCC ACCAACTGTC CATGGTACAA GGGTTGGACT AAGGAAACCA | 180 |
| AGGCAGGTGT TGTTAAGGGT AAGACCTTAT TAGAAGCAAT CGATGCTATT GAACCACCTG | 240 |
| TCAGACCAAC CGAAAAGCCA TTAAGATTAC CATTACAAGA TGTTTACAAG ATTGGTGGTA | 300 |
| TTGGTACTGT GCCAGTCGGT AGAGTCGAAA CCGGTGTCAT TAAGCCAGGT ATGGTTGTCA | 360 |
| CTTTTGCTCC AGCAGGTGTC ACCACCGAAG TCAATCCGT TGAATGCAC CATGAACAA | 420 |
| TAGAACAAAG TGTTCCAGGT GATAACGTTG GTTTCACGT TAAGAACGTY TCTGTCAAAG | 480 |
| ATATCAAGAG AGGTAACGTT TGTGGTGAAT CCAAGAACGA CCCACCAATG GGTGCAGCTT | 540 |
| CTTTCAATGC TCAAGTCATT GTCTGAACC ACCCTGGTCA AATTTCGCT GGTACTCTC | 600 |
| CAGTCTTGA TGTGCACACT GCCCACATTG CATGTAAGTT CGACGAATTA ATCGAAAAGA | 660 |
| TTGACAGAAG AACTGGTAAG TCTGTTGAAG ACCATCCAAA GTCYGTCAAG TCTGGTGATG | 720 |
| CAGCTATCGT CAAGATGGTC CCAACCAAGC CA | 752 |

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

| | |
|---|-----|
| CTCAGTCAAA TGGGACAAGA RCAGATACGA AGAAATTGTC AAGGAAACTT CCAACTTCGT | 60 |
| CAAGAAGGTT GGTTACAACC CTAAAGCTGT CCCATTGTC CCAATCTCTG GTTGGAACGG | 120 |
| TGACAATATG ATTGAACCAT CAACCAACTG TCCATGGTAC AAGGGTTGGG AAAAGGAAAC | 180 |
| TAAAGCTGGT AAGGTTACCG GTAAGACCTT GTTGAAGCT ATCGATGCTA TCGARCCACC | 240 |

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(2) INFORMATION FOR SEQ ID NO: 124:

(A) LENGTH: 753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

| | | | | | | |
|-------------|-------------|------------|-------------|------------|------------|-----|
| TCTGTTAAAT | GGGACAARAA | CAGATTTGAA | GAAATTATCA | AGGAACCYTC | TAACTTCGTC | 60 |
| AAGAAGGT TG | GTTACAACCC | TAAGGCTGTT | CCATTCTGTC | CAATCTCWGG | TTGGAATGGT | 120 |
| GACAACATGA | TTGAAGCTTC | TACCAACTGT | CCATGGTACA | AGGGTTGGGA | AAAAGAAACC | 180 |
| AAGGCTG GTA | AGGTTACCGG | TAAGACTTTG | TTGGAAGCCA | TTGATGCTAT | TGAACCACTT | 240 |
| TCAAGACCAA | CTGACAAGCC | ATTGAGATTG | CCATTGCAAG | ATGTTTACAA | GATTGGTGGT | 300 |
| ATTGGTACTG | TGCCAGTCGG | TAGAGTTGAA | ACTGGTG TCA | TCAAGCCGG | TATGGTTGTT | 360 |
| ACTTTYGCCC | CAGCTGGTGT | TACCACTGAA | GTCAAATCCG | TYGAAATGCA | CCACGAACAA | 420 |
| TTGSGTGAAG | GTGTCCCAGG | TGACAATGTT | GGTTTCAACG | TTAAGAACGT | TTCTGTTAAA | 480 |
| GAAATTAGAA | GAGGTAA CGT | TTGTGGTGAC | TCCAAGAACG | ATCCACCAAA | GGGTTGTGAC | 540 |
| TCTTTCAACG | CTCAAGTTAT | TGTCTTGAAC | CACCCAGGTC | AAATYCTGCG | TGGTTACTCT | 600 |
| CCAGTCTTGG | ATTGTGCAC | TGCTCATATT | GCTTGTA AAT | TCGACACCTT | GGTTGAAAAG | 660 |
| ATTGACAGAA | GAACTGGTAA | GAAATTGGAA | GAAATCCAA | AATTCGTCAA | ATCCGGTGAT | 720 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium accolens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

| | | | | | | |
|-------------|------------|-------------|-------------|------------|------------|-----|
| CGCGCGCTATC | CTGGTTGTTG | CTGCAACCGA | TGGCCCCGATG | CCGCAGACCC | GCGAGCACGT | 60 |
| TCTGCTTGCT | GCCACGGTTG | GCGTTCCTTA | CATCCTCGTT | GCACTGAACA | AGTGCACAT | 120 |
| GGTTCATGAT | GAGGAAATCA | TCGAGCTCGT | GGAGATGGAG | ATCTCCGAGC | TGCTCGCAGA | 180 |
| GCAGGACTAC | GATGAGGAAG | CTCCTATCGT | TCACATCTCC | GCTCTGAAGG | CACTCGAGGG | 240 |
| TGACGAGAAG | TGGGTACAGT | CCATCGTTGA | CCTGATGGAT | GCCTGCGACA | ACTCCATCCC | 300 |
| TGATCCGGAG | CGCGCTACCG | ATCAGCCGTT | CTTGATGCCT | ATCGAGGACA | TCTTCACCAT | 360 |
| TACCGGCCGC | GGTACCGTTG | TTACCGGCCG | TGTTGAGCGT | GGTCGTCTGA | ACGTCAACGA | 420 |
| GGACGTTGAG | ATCATCGGTA | TCCAGGAGAA | GTCCCAGAAC | ACCACCGTTA | CCGGTATCGA | 480 |
| GATGTTCCGC | AAGATGATGG | ACTACACCGA | GGCTGGCGAC | AACTGTGGTC | TGCTTCTGCG | 540 |
| TGGTACCAAG | CGTGAGGACG | TTGAGCGTGG | CCAGGTTGTT | ATCAAGCCGG | GCGCTTACAC | 600 |
| CCCTCACACC | AAGTTCGAGG | GTTCCGCTCA | CGTCTGAAG | AAGGAAGAGG | GCGGCCGCCA | 660 |
| CACCCCGYTC | ATGAACAAC | ACCGTCTCTCA | GTTCTACTTC | CGCACCACCG | ACGTTACCGG | 720 |
| TGTTGTGAAC | CTGCCTGAGG | GCACCGAGAT | GTTTATGCCT | GGCGACAACG | TTGAGATGTC | 780 |
| TGTTGAGCTC | ATCCAGCCTG | TTGCTATGGA | CGAG | | | 814 |

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

| | |
|---|-----|
| CGGCGCAATC CTCGTTGTTG CTGCCACCGA CGGCCCAATG CCTCAGACCC GTGAGCACGT | 60 |
| TCTGCTCGCT CGCCAGGTCG GCGTTCCCTTA CATCCTCGTT GCTCTGAACA AGTGCACAT | 120 |
| GGTTGATGAT GAGGAAATCA TCGAGCTCGT CGAGATGGAG ATCCRTGAGC TGCTCGCTGA | 180 |
| GCAGGATTAC GACGAAGAGG CTCCAATCAT CCACATCTCC GCACTGAAGG CTCTTGAGGG | 240 |
| CGACGAGAAG TGGACCCAGT CCATCATCGA CCTCATGCAG GCTTGCKATG ATTCCATCCC | 300 |
| AGACCCAGAG CGTGAGACCG ACAAGCCATT CCTCATGCCT ATCGAGGACA TCITCACCAT | 360 |
| CACCGGCCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCTCCCTGA AGGTCAACGA | 420 |
| GGACGTCGAG ATCATCGGTA TCCGCGAGAA KGCTACCACC ACCACCGTTA CCGGTATCGA | 480 |
| GATGTTCCGT AAGCTTCTCG ACTACACCGA GGCTGGCGAC AACTGTGGTC TGCTTCTCCG | 540 |
| TGCGGTTAAG CGCGAAGACG TTGAGCGTGG CCAGGTTGTT GTTAAGCCAG GCGCTTACAC | 600 |
| CCCTCACACC GAGTTCGAGG GCTCTGTCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA | 660 |
| CACCCCATTC TTGCAAACT ACGGCCACA GTTCTACTTC CGCACCACCG ACGTTACCGG | 720 |
| TGTTGTGAAG CTTCCTGAGG GCACCGAGAT GGTATGCCT GGCACAACG TCGACATGTC | 780 |
| CGTCACCCTG ATCCAGCCTG TCGCTATGGA TGAG | 814 |

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium genitalium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

| | |
|---|-----|
| CGGCGCCATC CTGGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT | 60 |
| TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCCTAGTT GCATGAACA AGTGCACAT | 120 |
| GGTTGATGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA | 180 |
| GCAGGACTTC GACGAGGAAG CACCTGTTGT TCACATCTCC GCATGAAGG CCCTGGAGGG | 240 |
| CGACGAGAAG TGGGCTAAGC AGATCCTGGA GTCATGGAG GCTTCGACA ACTCCATCCC | 300 |

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| | |
|---|-----|
| GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGRGGACA TCTTCACCAT | 360 |
| TACCGGCCCG GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCCTCCTGA ACCTGAACGA | 420 |
| CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG ACCACCGTTA CCTCCATCGA | 480 |
| GATGTTCAAC AAGTGTCTGG ACACCGCAGA GGCTGGCGAC AACGCCGCAC TGCTGCTGCG | 540 |
| TGGCCTGAAG CGCGAAGATG TTGAGCGTGG TCAGATCGTT GCTAAGCCGG GCGAGTACAC | 600 |
| CCCGCACACC GAGTTCGAGG GCTCCGCTA CGTTCTGTCC AAGGACGAGG GTGGCCGCCA | 660 |
| CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTATTTC CGCACCACCG ACGTTACCGG | 720 |
| TGTTGTGAAG CTGCGGAGG GCACCGAGAT GGTATGCGG GGCACACAAC TTGACATGTC | 780 |
| CGTCAACCTG ATCCAGCCGG TTGCTATGGA CGAG | 814 |

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium jeikeium*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

| | |
|---|-----|
| CGGCGCCATC CTGGTTGTG CCGCAACCGA TGGCCCGATG CCGCAGACCC GCGAGCACGT | 60 |
| TCTGCTGGCY CGCCAGGTTG GCGTCCGTA CATCCTGGTT GCACTGAACA AGTGTGACAT | 120 |
| GGTGACGAT GAGGAGCTGC TGGAGCTCGT CGAGATGGAG GTCCGCGAGC TGCTGGCTGA | 180 |
| GCAGGACTTC GACGAGGAAG CTCGGTGTGT TCACATCTCC GCACTGAAGG CCCTGGAGGG | 240 |
| CGACGAGAAG TGGGCTAACC AGATTCTCGA GCTGATGCAG GCTTGCAGAC AGTCTATCCC | 300 |
| GGATCCGGAG CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGWGGACA TCTTCACCAT | 360 |
| TACCGTTCGC GGTACCGTTG TTACCGGCCG TGTGAGCGT GGCATCCTGA ACCTGAACGA | 420 |
| CGAGGTTGAG ATCCTGGGTA TCCGCGAGAA GTCCCAGAAG ACCACCGTTA CCTCCATCGA | 480 |
| GATGTTCAAC AAGTGTCTGG ACACCGCAGA GGCTGGCRAC AACGCTGCAC TGCTGCTGCG | 540 |
| TGGTCTGAAG CGCGAGGACG TTGAGCGTGG CCAGATCATC GCTAAGCCGG GCGAGTACAC | 600 |
| CCCGCACACC GAGTTCGAGG GCTCCGCTA CGTTCTGTCC AAGGACGAGG GCGGCCGCCA | 660 |
| CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGCACCACCG ACGTTACCGG | 720 |

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814

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 748 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

748

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 813 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

| | | | | | | |
|-------------|------------|------------|-------------|------------|-------------|-----|
| GCGCGCTATCT | TGGTTGTTGC | TGCAACCGAT | GGCCCGRTGC | CGCAGACCCG | CGAGCACGTT | 60 |
| CTTCTGGCTC | GCCAGGTTGG | CGTTCCTTAC | ATCTCTCGTTG | CACTGAACAA | GTGCGCATATG | 120 |
| GTTGACGACG | AGGAAATTAT | CGAGCTCGTC | GAGATGGAGA | TCCGCGAACT | GCTCGCAGAG | 180 |
| CAGGACTACG | ATGAGGAAGC | TCCGATCGTT | CACATCTCTG | CTCTGAAGGC | TCTTGAGGGC | 240 |
| GRCGAGAAGT | GGGTACAGGC | TATCGTTGAC | CTGATGCAGG | CTTGCGATGA | TCCATCCCCG | 300 |
| GATCCGGAGC | GCGAGCTGGA | CAAGCCGTTT | CTGATGCCAA | TCGAGGACAT | CTTCACCATC | 360 |
| ACCGGCCGCG | GTACCGTTGT | TACTGGCCGT | GTTGAGCGTG | GCTCCCTGAA | CGTCAACGAG | 420 |
| GACGTTGAGA | TCATCGGTAT | CCAGGACARG | TCCATCTCCA | CCACCGTTAC | CGGTATCGAG | 480 |
| ATGYTCCGCA | AGATGATGGA | CTACACCGAG | GCTGGCGACA | ACTGTGGTCT | GCTTCTGCGT | 540 |
| GGTACCAAGC | GTGAAGAGGT | TGAGCGCGGC | CAGGTTGTTA | TTAAGCCGGG | CGCTTACACC | 600 |
| CCTCACACCC | AGTTCGAGGG | TTCCGTCTAC | GTCCCTGAAG | AGGAAGAGGG | CGGCCGCCAC | 660 |
| ACCCCGTTCA | TGGACAACCT | CCGTCGCGAG | TTCTACTTCC | GCACCACCGA | CGTTACCGGC | 720 |
| GTCATCAAGC | TGCCTGAGGG | CACCGAGATG | GTTATGCCTG | GCGACAACGT | CGAGATGTCY | 780 |
| GTCGAGCTGA | TCCAGCCGGT | CGCTATGGAC | GAG | | | 813 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

| | | | | | | |
|------------|------------|------------|------------|-------------------------|--------------------------|-----|
| CGGAGCTATC | TTAGTAGTAT | CTGCTGCTGA | TGGCCCTATG | CCTCAAACCT | GTGAACACAT | 60 |
| CTTGTTATCT | CGTAACGTTG | GTGTTCCTTA | CATCGTTGTA | TTC ⁺ TAAACA | AAATGGATAT | 120 |
| GGTGTACGAT | GAAGAATTAC | TTGAATTAGT | TGAAATGGAA | GTTCTGTACT | TATTA ⁺ ACTGA | 180 |
| ATACGACTTC | CCAGGCGACG | ACACTCCAGT | TATCGCAGGT | TCACGCTTGA | AAGCTTTAGA | 240 |
| AGGCGACGCT | TCATACGAAG | AAAAAATCTT | AGAATTAATG | GCTGCTGTTG | ACGAATATAT | 300 |

(2) INFORMATION FOR SEQ ID NO: 132:

- | | | | | | | | | |
|------------|------------|------------|------------|------------|-------------|------------|------------|-----|
| CGGAGCTATC | TTAGTAGT | TTCTGCTG | TGGTCC | TATG | CCTCAAAC | AC | GTGAACATAT | 60 |
| CTTATTATCA | CGTAACGTT | G | GTGTACCATA | CATCGTTGTA | TTCTTAAACA | AAATGGATAT | | 120 |
| GGTTGATGAC | GAAGAATTAT | TAGAATTAGT | AGAAATGGAA | GTTCGTGACT | TATTATCAGA | | | 180 |
| ATACGATTTC | CCAGGCGATG | ATGTTCCAGT | TATCGCAGGT | TCTGCTTIGA | AAGCTTTAGA | | | 240 |
| AGGCGACGAG | TCTTATGAAG | AAAAAATCTT | AGAATTAATG | GCTGCAGTTG | ACGAATATAT | | | 300 |
| CCCAACTCCA | GAACGTGATA | CTGACAAACC | ATTCATGATG | CCAGTCGAAG | ACGTATTCTC | | | 360 |
| AATCACTGGA | CGTGGTACTG | TTGCTACAGG | ACGTGTTGAA | CGTGGTGAAG | TTCCGCGTTGG | | | 420 |
| TGACGAAGTT | GAAATCGTTG | GTATTAAAGA | CGAAACATCT | AAAACAACYG | TTACAGGTGT | | | 480 |
| TGAAATGTTT | CGTAAATTAT | TAGACTACGC | TGAAGCAGGC | GACAACTCG | GTGCTTTATT | | | 540 |
| ACGTGGTGTA | GCACGTGAAG | ATATCGAACG | TGGACAAGTA | TTAGCTAAAC | CAGCTACAAT | | | 600 |
| CACTCCACAC | ACAAAATTC | AAGCTGAAGT | ATACGTATTA | TCAAAGAAG | AAGGCGGACG | | | 660 |
| TCACACTCCA | TTCTTCACTA | ACTACCGTCC | TCAATTCTAC | TTCCGTACAA | CAGACGTTAC | | | 720 |

(2) INFORMATION FOR SEQ ID NO: 133:

- | | | | | | | |
|-------------|-------------|------------|-------------|------------|-------------|-----|
| CGGAGCATATC | TTGGTAGTIT | CTGCTGCTGA | CGGCCCAATG | CCTCAAACCT | GTGAACACAT | 60 |
| CCTATITGCT | CGTCAAGTTG | GTGTTCTCTA | CATCGTITGA | TTCTTGAACA | AAGTAGACAT | 120 |
| GGTTGATGAC | GAAGAATTAC | TAGAATTAGT | TGAAATGGAA | GTTCTGTACC | TATTAACAGA | 180 |
| ATACRAATTC | CCTGGTGRGC | ATGTTCTCTG | AGTTGTCTGA | TCAGCTTTGA | AAGCTCTAGA | 240 |
| AGGCGACGCT | TCATACGAAG | AAAAAATTCT | TGAATTAATG | GCTGCAGTTG | ACGAATACAT | 300 |
| CCCAACTCCA | GAACGTGACA | ACGACAAACC | ATTCATGATG | CCAGTTGAAG | ACGTGTTCTC | 360 |
| AATTACTGGA | CGTGGTACTG | TTGCTACAGG | TCGTGTTGAA | CGTGGACAAG | TTCGCGTTGG | 420 |
| TGACGAAGTT | GAAGTTGTTG | GTATTGCTGA | AGAACTTCA | AAAACAACAG | TTACTGGTGT | 480 |
| TGAAATGTTT | CGTAAATTGT | TAGACYACGC | TGAAGCTGGA | GACRACATTG | GTGCTTTACT | 540 |
| ACGTGGTGTT | GCACGTGAAG | ACATCCAACG | TGGACAAGTT | TTAGCTAAAC | CAGGTACAAAT | 600 |
| CACACCTCRT | ACAAAATCTT | CTGCAGAAGT | ATACGTGTTG | ACAAAAGAAG | AAGGTGGAAG | 660 |
| TCATACTCCA | TTCTTCACTA | ACTACCGTCC | ACAATTTCTAC | TTCCGTACAA | CTGACGTAAC | 720 |
| AGGTGTTGTT | GAATTACCAAG | AAGGAACTGA | AATGGTCATG | CCCGGTGACA | ACGT | 774 |

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

| | |
|--|-----|
| CGGTGCGATC TTAGTAGTAT CTGCTGCTGA CGGTCCTATG CCTCAAACCTC GTGAACACAT | 60 |
| CTTGTIATCA CGTAACGTTG GCGTACCATA CATCGTTGTT TTCTTGAACA AAATGGATAT | 120 |
| GGTTGAYGAC GAAGAATTGC TAGAATTAGT TGAATGGAA GTTCGTGACC TATTGTCTGA | 180 |
| ATATGACTTC CCAGGCGACG ATGTTCTCTGT AATCGCCGGT TCTGCTTTGA AAGCTCTTGA | 240 |
| AGGAGATCCT TCATACGAAG AAAAAATCAT GGAATTGATG GCTGCACTTG ACGAATACGT | 300 |
| TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCACTCGAAG ACGTATTCTC | 360 |
| AATCACTGGA CGTGTACTG TTGCTACAGG CCGTGTGTA GCGTGACAAG TTCGCGTTGG | 420 |
| TGATGAAGTA GAAATCGITG GTATTGCTGA CGAAACTGCT AAAACAACCTG TAACAGGTGT | 480 |
| TGAAATGTTT CGTAAATTGT TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT | 540 |
| ACGTGGGGTT GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACAAT | 600 |
| CACACCTCAT ACAAATTC AAGCTGAAGT TTATGTTTTG ACAAAGAAG AAGGTGGAAG | 660 |
| TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| TGTTGTTGTT GAATTACCAG AAGGAACTGA AATGGTGATG CCTGGCGACA ACGTGACCAT | 780 |
| CGACGTTGAA TTGATRCACC CAATCGCTC | 809 |

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gardnerella vaginalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

| | |
|---|-----|
| TGGCGCAATC CTCGTGGTTG CTGCTACCGA CGGTCCAATG GCTCAGACCC GTGAACACGT | 60 |
| CTTGCTTGCT AAGCAGGTGC GCGTTCCAAA AATTCTTGTT GCTTTGAACA AGTGCATAT | 120 |
| GGTTGACGAC GAAGAGCTTA TCGATCTCGT TGAAGAAGAG GTCCGTGACC TCCTCGAAGA | 180 |
| AAACGGCTTC GATCGCGATT GCCCAGTCYT CCGTACTTCC GCTTACGGCG CTTTGCATGA | 240 |
| TGACGCTCCA GACCACGACA AGTGGGTAGA GACCGTCAAG GAACTCATGA AGGCTGTTGA | 300 |

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| | |
|---|-----|
| CGAGTACATC CCAACCCCAA CTCACGATCT TGACAAGCCA TTCTTGATGC CAATCGAAGA | 360 |
| TGTGTTACAC ATCTCCGGTC GTGGTYCCGT TGTACCCGT CGTGTGAGC GTGSTAAGCT | 420 |
| CCCAATCAAC ACCCCAGTTG AGATCGTTGG TTTGCGCGAT ACCCAGACCA CCACCGTCAC | 480 |
| CTCTATCGAG ACCTTCCACA AGCAGATGGA TGAGGCAGAG GCTGGCGATA ACATGGTCT | 540 |
| TCTTCTCCGC GGTATCAACC GTACCGACGT TGAGCGTGGT CAGGTTGTGG CTGCTCCAGG | 600 |
| TTCTGTGACT CCACACACCA AGTTCGAAGG CGAAGTTTAC GTCTTGACCA AGGACGAAGG | 660 |
| TGGCCGTCAC TCGCCATTCT TCTCCAACCT CCGTCCACAG TTCTACTTCC GTACCACCGA | 720 |
| TGTTACTGGC GTTATCACCT TGCCAGACGG CATCGAAATG GTTCAGCCAG GCGATCACGC | 780 |
| AACCTTCACT GTTGAGTTGA TCCAGGCTAT CGCAATGGAA GAG | 823 |

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria innocua*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

| | |
|--|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCAATGAACA AATGTGACAT | 120 |
| GGTTCAGCAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |
| AGGTGAAGCT GACTGGGAAG CTAATAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT | 300 |
| TCCAACTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC | 360 |
| AATCACTGGT CGTGGAACAG TTGCAACTGG ACGTGTGAA CGTGGAACAAG TTAAGATTGG | 420 |
| TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAGCAAA AAGTAGTAG TAAGTGGAGT | 480 |
| AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT | 540 |
| ACGTGTTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTTCGAT | 600 |
| TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTAA ACTAAGAAG AAGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC | 720 |

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(2) INFORMATION FOR SEQ ID NO: 137:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

(2) INFORMATION FOR SEQ ID NO: 138:

- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT | 120 |
| GGTGACGAT GAAGAATTAC TAGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGCGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |
| AGGTGAAGCT GACTGGGAAG CTAAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT | 300 |
| TCCAACTCCW GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC | 360 |
| AATCACTGGT CGTGAACAG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG | 420 |
| TGACGAAGTA GAAGTTATCG GTATCGAAGA AGAAAGCAAA AAAGTAGTAG TAACTGGAGT | 480 |
| AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT | 540 |
| ACGTGGTGT GTCGTGAAG ATATCCAACR TGSTCAAGTA TTAGCTAAAC CAGGTTGAT | 600 |
| TACTCCACAC ACTAACTTCA AAGCTGAAAC TTATGTTTAA ACTAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACGCCC ACAATTCTAT TTCCGTACTA CTGACGTAAC | 720 |
| TGGTATTGTT ACACCTCCAG AAGGTACTGA AATGGTAAYG CCTGGTGATA ACATTGAGCT | 780 |
| TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC | 817 |

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria seeligeri*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACATAT | 60 |
| CTTACTTTCA CGTCAAGTTG GTGTTCCATA CATCGTTGTA TTCATGAACA AATGTGACAT | 120 |
| GGTGACGAT GAAGAATTAC TTGAATTAGT TGAAATGGAA ATTCGTGATC TATTAAGTGA | 180 |
| ATATGAATTC CCTGGTGATG ACATTCCTGT AATCAAAGGT TCAGCTCTTA AAGCACTTCA | 240 |

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| | |
|---|-----|
| AGGTGAAGCT GACTGGGAAG CTA AAAATTGA CGAGTTAATG GAAGCTGTAG ATTCTTACAT | 300 |
| TCCAACCTCCA GAACGTGATA CTGACAAACC ATTCATGATG CCAGTTGAGG ATGTATTCTC | 360 |
| AATCACTGGT CGTGGAACTG TTGCAACTGG ACGTGTGAA CGTGGACAAG TTAAAGTTGG | 420 |
| TGACGAAGTA GAAGTTATCG GTATTGAAGA AGAAAGCAAA AAAGTAATAG TAACTGGAGT | 480 |
| AGAAATGTTT CGTAAATTAC TAGACTACGC TGAAGCTGGC GACAACATTG GCGCACTTCT | 540 |
| ACGTGGTGTT GCTCGTGAAG ATATCCAACG TGGTCAAGTA TTAGCTAAAC CAGGTTGAT | 600 |
| TACTCCACAT ACTAATTCA AAGCTGAAAC TTATGTTTTA ACTAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCCTCAACA ACTACGCCC ACAATTCTAT TTCCGTTACTA CTGACGTAAC | 720 |
| TGTTATTGTT ACACCTCCAG AAGGTACTGA AATGGTAATG CCTGGTGATA ACATTGAGCT | 780 |
| TGCAGTTGAA CTAATTGCAC CAATCGCTAT CGAAGAC | 817 |

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

| | |
|--|-----|
| CGGTGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC GTGAACACAT | 60 |
| TCITTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA TTCTTAAACA AAGTTGACAT | 120 |
| GGTTGACGAT GAAGAATTAT TAGAATTAGT AGAAATGGAA GTTCGTGACT TATTAAGCGA | 180 |
| ATATGACTTC CCAGTGACG ATGTACCTGT AATCGCTGGT TCAGCATTAR AAGCTTAGA | 240 |
| AGGCGATGCT CAATACGAAG AAAAAATCTT AGAATTARTG GAAGCTGTAG ATACTTACAT | 300 |
| TCCAACCTCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC | 360 |
| AATCACTGGT CGTGTACTG TTGCTACAGG CCGTGTGAA CGTGGTCAA TCAGAGTTGG | 420 |
| TGAAGAAGTT GAAATCATCG GTTTACATGA CACATCTAAA ACAACTGTTA CAGGTGTTGA | 480 |
| AATGTTCCTG AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATTGGTG CATTATTACG | 540 |
| TGGTGTTGCT CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC | 600 |
| ACCACATACT GAATTCAAAG CAGAAGTATA CGTATTATCA AAAGACGAAG GTGACGCTCA | 660 |

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| | |
|--|-----|
| CACTCCATTTC TTCTCAAACCT ATCGTCCACA ATTCTATTTC CGTACTACTG ACGTAACTGG | 720 |
| TGTTGTTTCCAC TTACCAGAAG GTACTGAAAT GGTAAATGCCT GGTGATAACG TTGAAATGAC | 780 |
| AGTAGAATTA ATCGCTCCAA TCGCGATTGA AGAC | 814 |

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

| | |
|---|-----|
| CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC GTGAACACAT | 60 |
| CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT | 120 |
| GGTAGACGAC GAAGAATTAT TAGAATTAGT TGAATGGAA GTTCGTGACT TATTAAGCGA | 180 |
| ATATGACTTC CCAGGTGACG ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA | 240 |
| AGGCGATGCT GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT | 300 |
| TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAAGTGAAG ACGTATTCTC | 360 |
| AATCACTGGT CGTGGTACTG TTGCTACAGS CCGTGTGAA CGTGGTCAAA TCAAAGTWGG | 420 |
| TGAAGAAGTT GAAATCATCG GTATGCACGA AACTTCTAAA ACAACTGTTA CTGGTGTAGA | 480 |
| AATGTTCCGT AAATTATTAG ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG | 540 |
| TGGTGTGCA CGTGAAGACG TACAACGTGS TCAAGTATTA GCTGCTCCTG GTTCTATTAC | 600 |
| ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG GTGGACGTCA | 660 |
| CACTCCATTTC TCACTAACT ATCGCCCACT ATTCTATTTC CRTACTACTG ACGTAACTGG | 720 |
| TGTTGTAAC TTACCAGAAG GTACAGAAAT GGTATGCCT GGCACACAAC TTGAAATGAC | 780 |
| AGTTGAATTA ATCGCTCCAA TCGCTATCGA AGAC | 814 |

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

| | |
|---|-----|
| CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAAACTC GTGAACACAT | 60 |
| TCTTTTATCA CGTRACGTTG GTGYTCCAGC ATTAGTTGTA TTCTTAAACA AAGTTGACAT | 120 |
| GGTTGACGAY GAAGAATTAT TAGAATTTRGT AGAAATGGAA GTTCGTGRCT TATTAAGCGA | 180 |
| ATATGACTTC CCAGSTGACG ATGTACCTGT AATCTCTGGT TCTGCATTAA AAGCTTTAGA | 240 |
| AGGCGACGCT GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTYCAT | 300 |
| TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG ACGTATTCTC | 360 |
| AATCACTGGT CGTGCTACTG TTGCTACAGG CCGTGTGAA CGTGTCACAA TCAAAGTCGG | 420 |
| TGAAGAAATC GARATCATCG GTATGAAGA AGAATCAAGC AAAACAACCTG TTACTGGTGT | 480 |
| AGAAATGTTT CGTAAATTAT TAGACTACGC TGAAGCTGGT GACAACATTG GTGCATTATT | 540 |
| ACGTGGTGTT TCACGTGATG ATGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTACTAT | 600 |
| CACACCACAT ACAAATTTCA AAGCGGATGT TTACGTTTTA TCTAAAGATG AAGGTGGTCG | 660 |
| TCATACGCCA TTCTTCACTA ACTACCGCCC ACAATTCTAT TTCCGTTACTA CTGACGTAAAC | 720 |
| TGGTGTGTGT AACTTACCAG AAGGTACTGA AATGGTTATG CCTGGCGATA ACGTTGAAAT | 780 |
| GGATGTTGAA TTAATTTCTC CAATCGCTAT TGAAGAC | 817 |

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 817 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus simulans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

| | |
|---|-----|
| CGGCGGTATC TTAGTAGTAT CTGCTGCAGA TGGTCCAATG CCACAAACTC GTGAACACAT | 60 |
| CTTATTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA TTCTTAAACA AAGCTGACAT | 120 |
| GGTTGACGAC GAAGAATTAT TAGAATTAGT TGAATGGAA GTTCGTGACT TATTATCTGA | 180 |

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(2) INFORMATION FOR SEQ ID NO: 144:

(A) LENGTH: 817 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGAGCTATC | CTTGTAGTTG | CTTCAACTGA | TGGACCAATG | CCACAAACTC | GTGAGCACAT | 60 |
| CCTTCTTTCA | CGTCAAGTTG | GTGTTAAACA | CCTTATCGTA | TTCATGAACA | AAGTTGACCT | 120 |
| TGTTGATGAT | GAAGAATTGC | TTGAATTGGT | TGAAATGGAA | ATTCGTGACC | TTCTTTCAGA | 180 |
| ATACGACTTC | CCAGGTGATG | ACCTTCCAGT | TATCCAAGGT | TCAGCTCTTA | AAGCACTTGA | 240 |
| AGGCGACGAA | AAATACGAAG | ACATCATCAT | GGAATTGATG | AGCACTGTTG | ATGAGTACAT | 300 |
| TCCAGAACCA | GAACGTGATA | CTGACAAACC | TTTACTTCTT | CCAGTTGAAG | ATGATPTCTC | 360 |
| AATCACTGGA | CGTGGTACAG | TTGCTTCAGG | ACGTATCGAC | CGTGGTACTG | TTCGTGTCAA | 420 |
| CGACGAAGTT | GAAATCGTTG | GTATTAAAGA | AGATATCCAA | AAAGCAGTTG | TTACTGGTGT | 480 |
| TGAAATGTTT | CGTAAACAAC | TTGACGAAGG | TCTTGCAGGG | GACAACGTTG | GTGTTCTTCT | 540 |
| TCGTGGTGGT | CAACGTGATG | AAATCGAACG | TGGTCAAGTT | CTTGCTAAAC | CAGGTTCAAT | 600 |

| | |
|---|-----|
| CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG AAGGTGGACG | 660 |
| TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACAA CTGACGTAAC | 720 |
| AGGTTCAATC GAACTTCCAG CAGGAACAGA AATGGTTATG CCTGGTGATA ACGTTACTAT | 780 |
| CGAAGTTGAA TTGATTACC CAATCGCCGT AGAACAA | 817 |

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

| | |
|---|-----|
| CGGAGCTATC CTTGTAGTAG CTTCAACTGA CGGACCAATG CCACAAACTC GTGAGCACAT | 60 |
| CCTTCTTICA CGTCAGGTG GTGTTAAACA CCTTATCGTC TTCATGAACA AAGTTGACTT | 120 |
| GGTTGACGAC GAAGAATTGC TTGAATTGGT TGAATGGAA ATCCGTGACC TATTGTCAGA | 180 |
| ATACGACTTC CCAGGTGACG ATCTTCCAGT TATCCAAGGT TCAGCACTTA AAGCTCTTGA | 240 |
| AGGTGACTCT AAATACGAAG ACATCGTTAT GGAATTGATG AACACAGTTG ATGAGTATAT | 300 |
| CCCAGAACCA GAACGTGACA CTGACAAACC ATTGCTTCTT CCAGTCGAGG ACGTATTCTC | 360 |
| AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC CGTGGTATCG TTAAAGTCAA | 420 |
| CGACGAAATC GAAATCGTTG GTATCAAAGA AGAAACTCRA AAAGCAGTTG TTACTGGTGT | 480 |
| TGAAATGTTT CGTAAACAAC TTGACGAAGG TCTTGCTGGA GATAACGTAG GTGTCTTCT | 540 |
| TCGTGGTGTT CAACGTGATG AAATCGAACG TGGACAAGTT ATCGCTAAAC CAGGTTCAAT | 600 |
| CAACCCACAC ACTAAATTTA AAGGTGAAGT CTACATCCTT ACTAAAGAAG AAGGTGGACG | 660 |
| TCACACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC TTCCGTACTA CTGACGTTAC | 720 |
| AGGTTCAATC GAACTTCCAG CAGGTACTGA AATGGTAATG CCTGGTGATA ACGTGACAA | 780 |
| CGACGTTGAG TTGATTACC CAATCGCCGT AGAACAA | 817 |

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

(2) INFORMATION FOR SEQ ID NO: 147:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

AACATGATCA CCGGTGCTGC CGAGATGGAC GGCGCGATCC TGGTTTGCTC GGCTGCCGAC 60

GGCCCGATGC CACAGACCCG CGAGCACATC CTGCTTGCCC GTCAGGTGGG CGTTCGGGCC 120

(2) INFORMATION FOR SEQ ID NO: 148:

(A) LENGTH: 885 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus subtilis*

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ATGATCACTG | GTGCTGCGCA | AATGGACGGA | GCTATCCTTG | TAGTATCTGC | TGCTGATGGC | 60 |
| CCAATGCCAC | AAACTCGTGA | GCACATCCTT | CTTTCTAAAA | ACGTTGGTGT | ACCATACATC | 120 |
| GTGTGATTCT | TAAACAAATG | CGACATGGTA | GACGACGAAG | AGCTTCTTGA | ACTAGTTGAA | 180 |
| ATGGAAGTTC | GCGATCTTCT | TAGCGAATAC | GACTTCCTCG | GTGATGATGT | ACCAGTTGTT | 240 |
| AAAGGTTCTG | CTCTTAAAGC | TCTTGAAGGA | GACGCTGAGT | GGGAAGCTAA | AATCTTCGAA | 300 |
| CTTATGGATG | CGGTTGATGA | GTACATCCCA | ACTCCAGAAC | GCGACACTGA | AAAACCATTG | 360 |
| ATGATGCCAG | TTGAGGACGT | ATTCTCAATC | ACTGGTCGTG | GTACAGTTGC | TACTGGCCGT | 420 |
| GTAGAACGCG | GACAAAGTTAA | AGTCGGTGAC | GAAGTTGAAA | TCATCGGTCT | TCAAGAAGAG | 480 |

| | |
|---|-----|
| AACAAGAAAA CAACTGTTAC AGGTGTTGAA ATGTTCCGTA AGCTTCTTGA TTACGCTGAA | 540 |
| GCTGGTGACA ACATTGGTGC CCTTCTTCGC GGTGTATCTC GTGAAGAAAT CCAACGTGGT | 600 |
| CAAGTACTTG CTAAACCAGG TACAATCACT CCACACAGCA AATTCAAAGC TGAAGTTTAC | 660 |
| GTTCTTTCTA AAGAAGAGGG TGGACGTCAT ACTCCATTCT TCTCTAACTA CCGTCCTCAG | 720 |
| TTCTACTTCC GTACAACTGA CGTAACTGGT ATCATCCATC TTCCAGAAGG CGTAGAAATG | 780 |
| GTTATGCCTG GAGATAACAC TGAATGAAC GTTGAACTTA TTTCTACAAT CGCTATCGAA | 840 |
| GAAGGAACTC GTTTCTCTAT TCGTGAAGGC GGACGTACTG TTGGT | 885 |

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides fragilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

| | |
|---|-----|
| ATGGTTACTG GTGCTGCTCA GATGGACGGT GCTATCATTG TAGTTGCTGC TACTGATGGT | 60 |
| CCGATGCCTC AGACTCGTGA GCACATCCTT TTGGCTCGTC AGGTAACGT TCCGAAGCTG | 120 |
| GTTGTATTCA TGAACAAGTG CGATATGGTT GAAGATGCTG AGATGTTGGA ACTTGTTGAA | 180 |
| ATGGAATGA GAGAATTGCT TTCATTCTAT GATTTGACG GTGACAATAC TCCGATCATT | 240 |
| CAGGGTTCTG CTCTTGCTGC ATTGAACGGC GTAGAAAAAT GGGGAAGCAA AGTAATGGAA | 300 |
| CTGATGGAAG CTGTTGATAC TTGGATTCCA CTGCCTCCGC GCGATGTTGA TAAACCTTTC | 360 |
| TTGATGCCGG TAGAAGACGT GTTCTCTATC ACAGGTCGTG GTACTGTAGC TACAGGTCGT | 420 |
| ATCGAAACTG GTGTTATCCA TGTAGGTGAT GAAATCGAAA TCCTCGGTTT GGGTGAAGAT | 480 |
| AAGAAATCAG TTGTAACAGG TGTTGAAATG TTCCGCAAC TTCTGGATCA GGGTGAAGCT | 540 |
| GGTGACAACG TAGGTCTGTT GCTTCGTGGT GTTGACAAGA ACGAAATCAA ACGTGGTATG | 600 |
| GTTCTTTGTA AACCGGTGTA GATTAAACCT CACTCTAAAT TCAAAGCAGA GGTTTATATC | 660 |
| CTGAAGAAAG AAGAAGGTGG TCGTCACACT CCATTCCATA ACAAATATCG TCCTCAGTTC | 720 |
| TACCTGCGTA CTATGGACTG TACAGGTGAA ATCACTCTTC CGGAAGGAAC TGAAATGGTA | 780 |
| ATGCCGGGTG ATAACGTAAC TATCACTGTA GAGTTGATCT ATCCGGTTGC ACTGAACATC | 840 |

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GGTCITCGTT TCGCTATCCG CGAAGGTGGA CGTACAGTAG GT

882

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

| | |
|--|-----|
| AATATGATTA CAGGAGCAGC TCAAAATGGAT GCAGCGATAC TTTTAGTTGC TGCTGATAGT | 60 |
| GGTGTCTGAGC CTCAAACAAA AGAGCATTTG CTTCTTGCTC AAAGAATGGG AATAAAGAAA | 120 |
| ATAATAGTTT TTTTAAATAA ATTGGACTTA GCAGATCCTG AACTTGTTGA GCTTGTGAA | 180 |
| GTTGAAGTTT TAGAACTTGT TGAAAAATAT GGCTTTTCAG CTGATACTCC AATAATCAAA | 240 |
| GGTTCAGCTT TTGGGGCTAT GTCAAATCCA GAAGATCCTG AATCTACAAA ATGCGTTAAA | 300 |
| GAACCTCTTG AATCTATGGA TAATTATTTT GATCTTCAG AAAGAGATAT TGACAAGCCA | 360 |
| TTTTTGCTTG CTGTTGAAGA TGTATTTTCT ATTTTCAGAA GAGGCACTGT TGCTACTGGG | 420 |
| CGTATTGAAA GAGGTATTAT TAAAGTTGGT CAAGAAGTTG AAATAGTTGG AATTAAGAA | 480 |
| ACCAGAAAAA CTA CTGTTAC TGGTGTGAA ATGTTCCAGA AAATCTTGA GCAAGGTCAA | 540 |
| GCAGGGGATA ATGTTGTGCT TCTTTTGAGA GCGTTGATA AAAAGACAT TGAGAGGGGG | 600 |
| CAAGTTTGT CAGCTCCAGG TACAATTACT CCACACAAGA AATTTAAAGC TTCAATTTAT | 660 |
| TGTTTGACTA AAGAAGAAGG CGGTAGGCAC AAGCCATTTT TCCAGGGTA TAGACCACAG | 720 |
| TTCTTTTTTA GAACAACCGA TGTTACTGGA GTTGTGCTT TAGAGGGCAA AGAAATGGTT | 780 |
| ATGCCTGGTG ATAATGTTGA TATTATTGTT GAGCTGATCT CTTCATAGC TATGGATAAG | 840 |
| AATGTAGAAT TTGCTGTTG AGAAGGTGGA AGAACCGTTG CTCAGGA | 888 |

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Brevibacterium linens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

| | |
|---|-----|
| AACATGATCA CCGTGCCGC TCAGATGGAC GGTGCGATCC TCGTCGTCGC CGCTACCGAC | 60 |
| GGACCGATGC CCCAGACCCG TGAGCACGTG CTGCTCGCGC GTCAGGTCGG CGTTCCCTAC | 120 |
| ATCGTCGTGG CTCTGAACAA GTCCGACATG GTCGATGACG AGGAGCTCCT CGAGCTCGTC | 180 |
| GAATTCGAGG TCCGCGACCT GCTCTCGAGC CAGGACTTCG ACGGAGACAA CGCTCCGGTC | 240 |
| ATTCCGGTGT CCGCTCTCAA GGCCTGGA GGCAGCAGA AGTGGGTCAA GAGCGTTCAG | 300 |
| GATCTCATGG CTGCCGTCGA TGACAACGTT CCGGAGCCGG AGCGCGATGT CGACAAGCCG | 360 |
| TTCTCATGC CCGTCGAGGA CGTCTTCACG ATCACCGGTC GTGGAACCGT CGTCACCGGT | 420 |
| CGTGTGAGC GCGGCGTGCT CCTGCCTAAC GACGAAATCG AAATCGTCGG CATCAAGGAG | 480 |
| AAGTCGTCCA AGACGACTGT CACCGCTATC GAGATGTTCC CCAAGACCCT GCCGGATGCC | 540 |
| CGTGAGGTG AGAACGTCGG TCTGCTCCTC CGCGGCACCA AGCGCGAGGA TGTTGAGCGC | 600 |
| GGTCAGGTCA TCGTGAAGCC GGGTTCGATC ACCCCGCACA CCAAGITCGA GGCTCAGGTC | 660 |
| TACATCTGA GCAAGGACGA GGGCGGACGT CACAACCCGT TCTACTCGAA CTACCGTCCG | 720 |
| CAGTTCTACT TCCGGACCAC GGACGTCACC GGTGTCATCA CGCTGCCCGA GGGCACCAGG | 780 |
| ATGGTCATGC CCGGCGACAA CACCGATATG TCGGTCGAGC TCATCCAGCC GATCGCTATG | 840 |
| GAGGACCGCC TCCGCTTCGC AATCCGCGAA GGTGGCCGCA CCGTCGGCGC CGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

| | |
|---|-----|
| ATGATCACGG GCGCAGCGCA GATGGACGGC GCGATCCTGG TTTGCTCGGC AGCAGACGGC | 60 |
| CCGATGCCCG AAACGCGTGA GCACATCCTG CTGGCGCGTC AGGTTGGTGT TCCGTACATC | 120 |
| ATCGTGTTC TGAACAAGTG CGACAGTGTG GACGACGCTG AACTGCTCGA GCTGGTCGAG | 180 |

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| | |
|--|-----|
| ATGGAAGTTC GCGAACTCCT GTCGAAGTAC GACTTCCC GG GCGACGACAC GCCGATCGTG | 240 |
| AAGGGTTCGG CCAAGCTGGC GCTGGAAGGC GACACGGGCG AGCTGGGCGA AGTGGCGATC | 300 |
| ATGAGCCTGG CAGACGCGTG GGACACGTAC ATCCCGACGC CGGAGCGTGC AGTTGACGGC | 360 |
| GCGTTCCTGA TGCCGGTGGA AGACGTGTTC TCGATCTCGG GCCGTGGTAC GGTGGTGACG | 420 |
| GGTCGTGTGC AGCGCGGCAT CGTGAAGGTC GGCGAAGAAA TC GAAATCGT CGGTATCAAG | 480 |
| CCGACGGTGA AGACGACCTG CACGGGCGTT GAAATGTTC GCAAGCTGCT GGACCAAGGT | 540 |
| CAGGCAGGCG ACAACGTCGG TATCCTGCTG CGCGGCACGA AGCGTGAAGA CGTGAGCGT | 600 |
| GGCCAGGTTC TGGCGAAGCC GGGTTCGATC ACGCCGCACA CGCACTTCAC GGCTGAAGTG | 660 |
| TACGTGCTGA GCAAGGACGA AGGCGGCCGT CACACGCCGT TCTTCAACAA CTACCGTCCG | 720 |
| CAGTTCTACT TCCGTACGAC GGACGTGACG GGCTCGATCG AGCTGCCGAA GGACAAGGAA | 780 |
| ATGGTGATGC CGGGCGACAA CGTGTCGATC ACGGTGAAGC TGATTGCTCC GATCGCGATG | 840 |
| GAAGAAGGTC TGCCTTCGC AATCCGTGAA GGCGGCCGTA CGGTCCGG | 888 |

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

| | |
|--|-----|
| AACATGATCA CCGGTGCGGC TCAAATGGAC GGGGCTATTC TAGTAGTTTC TGCAACAGAC | 60 |
| GGAGCTATGC CTCAAATAA AGAGCATATT CTTTGGCAA GACAAGTTGG GGTTCCTTAC | 120 |
| ATCGTTGTTT TTCTCAATAA AATTGACATG ATTTCCGAAG AAGACGCTGA ATTGTCGAC | 180 |
| TTGGTTGAGA TGGAGTTGGC TGAGCTTCTT GAAGAGAAA GATACAAAGG GTGTCCAATC | 240 |
| ATCAGAGGTT CTGCTCTGAA AGCTTTGGAA GGAGATGCTG CACATAGTA GAAAGTTGCA | 300 |
| GAGCTAATGC AAGCCGTCGA TGATAATATC CCTACTCCAG AAGAGAGAAAT TGACAAGCCT | 360 |
| TTCTTAATGC CTATTGAGGA CGTGTCTCT ATCTCCGGAC GAGGAACTGT AGTAACTGGA | 420 |
| CGTATTGAGC GTGGAATTGT TAAAGTTTCC GATAAAGTTC AGTTGGTCGG TCTTAGAGAT | 480 |
| ACTAAGAAAA CGATTGTTAC TGGGGTTGAA ATGTTTCAGAA AAGAACTCCC AGAAGGTCGT | 540 |

| | |
|--|-----|
| GCAGSAGAGA ACGTTGGATT GCTCCTCAGA GGTATTGGTA AGAACGATGT GGAAAGAGGA | 600 |
| ATGGTTGTTT GCTTGCCAAA CAGTGTAAAA CCTCATAAC AGTTTAAGTG TGCTGTTTAC | 660 |
| GTTCTGCAAA AAGAAGAAGG TGGACGACAT AAGCCTTTCT TCACAGGATA TAGACCTCAA | 720 |
| TTCTTCTTCC GTACAACAGA CGTTACAGGT GTGGTAACCT TGCCAGAGGG AGTTGAGATG | 780 |
| GTCATGCCCTG GGGATAACGT TGAGTTTGAA GTGCAATTGA TTAGCCCTGT GGCCTTAGAA | 840 |
| GAAGGTATGA GATTTCGAT TCGTGAAGGT GGTCTGACAA TCGGTGCTGG A | 891 |

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

| | |
|---|-----|
| AACATGATCA CCGGTGCTGC GCAGATGGAC GGCSCGATCC TGGTAGTTGC TGCGACTSAC | 60 |
| GGCCCGATGC CGCAGACTCG TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCGGTAC | 120 |
| ATCATCGTGT TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT | 180 |
| GAAATGGAAG TTCGTGAAC TCTGTCTCAG TACGACTTCC CGGGCGACGA CACTCCGATC | 240 |
| GTTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCACGACAG AGTGGGAAGC GAAATCCTG | 300 |
| GAATGCGCTG GCTTCCTGGA TTCTTACATT CCGGAACCG AGCGTGCGAT TGACAAGCCG | 360 |
| TTCTGTGTCG CGATCGAAGA CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTACCGGT | 420 |
| CGTGAGAAC GCGGTATCAT CAAAGTTGGT GAAGAAGTTG AAATCGTTGG TATCAAAGAG | 480 |
| ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT | 540 |
| GCTGTTGAGA ACGTAGTGT TCTGCTGCGT GGTATCAAA GTGAAGAAAT CGAAGCTGGT | 600 |
| CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA AGTTCGAATC TGAAGTGTAC | 660 |
| ATTCTGTCCA AAGATGAAGG CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CGGTCCGCAG | 720 |
| TTCTACTTCC GTACTACTGA CGTGAAGTGT ACCATCGAAC TGCCGGAAGG CGTAGAGATG | 780 |
| GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT CGCGATGGAC | 840 |
| GACGGTCTGC GTTTCGCAAT CCGTGAAGGC GGCCTGACCG TTGGCGCGGG C | 891 |

0990643-112001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Fibrobacter succinogenes*

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| ACACATGGTGA | CTGGTGCTGC | TCAGATGGAC | GGCGCTATCC | TCGTTGTTGC | CGTACTGAC | 60 |
| GGTCCGATGC | CGCAGACTCG | CGAACACATC | CTTCTCGCTC | ACCAGGTTGG | CGTGCCGAAG | 120 |
| ATCGTCGTGT | TCATGAACAA | GTGCACATG | GTTGACGATG | CTGAAATTCT | CGACCTCGTC | 180 |
| GAAATGGAAG | TTCGCGAACT | CCTCTCCAAG | TATGACTTTC | ACGGTGACAA | CACCCCGATC | 240 |
| ATCCGTGTGGT | CCGCTCTCAA | GGCCCTCGAA | GGCGATCCGG | AATACCAGGA | CAAGGTCATG | 300 |
| GAACACTATGA | ACGCTTGCGA | CGAATACATC | CCGCTCCCGC | AGCGCGATAC | CGACAAGCCG | 360 |
| TTCTCTCATGC | CGATCGAAGA | CGTGTTCAAG | ATTACTGGCC | GCGGCACATG | CGTACTGGC | 420 |
| CGTATCGAAC | GCGGTGTCTG | TCGCTTGAAC | GACAAGGTTG | AACGATATCG | TCTCGGTGAA | 480 |
| ACCACCGAAT | ACGTATCATC | CGGTGTTGAA | ATGTTCCGTA | AGCTCCTCGA | CGACGCTCAG | 540 |
| GCAGGTGACA | ACGTTGGTCT | CCTCTCCCGT | GGTGCTGAAA | AGAAGGACAT | CGTCCGTGGC | 600 |
| ATGGTTTCTCG | CAGCTCCGAA | GTCTGTCACT | CCGCACACCG | AATTTAAGGC | TGAAATCTAC | 660 |
| GTCTCTCAGA | AGGACGAAGG | TGGCCGTCAC | ACGCCGTTCA | TGAATTGGCTA | CCGTCCGCAG | 720 |
| TTCTACTTCC | GCACCACCGA | CGTTACTGGT | ACGATCCAGC | TCCCGGAAGG | TGTCGAAATG | 780 |
| GTACTCTCGG | GTGACACGGT | CACGATCCAC | GTGAACCTCA | TCGCTCCGAT | CGCTATGGAA | 840 |
| AAGCAGCTCC | GCTTCGCTAT | CCGTGAAGGT | GGACGTACTG | TTGGTGCTGG | C | 891 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Flavobacterium ferrugineum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

| | |
|---|-----|
| AACATGATCA CCGTGCTGCG CCAGATGGAC GGTGCTATCT TAGTTGTGGC TGCATCAGAC | 60 |
| GGTCTTATGC CTCAAACAAA AGAACACATC CTGCTTGCTG CCCAGGTAGG TGTACCTAAA | 120 |
| ATGGTTGTGT TTCTGAATAA AGTTGACCTC GTTGACGACG AAGAGCTCCT GGAGCTGGTT | 180 |
| GAGATCGAGG TTCGCGAAGA ACTGACTAAA CGCGGTTTCG ACGGCGACAA CACTCCAATC | 240 |
| ATCAAAGGTT CCGCTACAGG CGCCCTCGCT GGTGAAGAAA AGTGGGTTAA AGAAATTGAA | 300 |
| AACCTGATGG ACGCTGTTGA CAGCTACATC CCACTGCCTC CTCGTCCGGT TGATCTGCCG | 360 |
| TTCCTGATGA GCGTAGAGGA CGTATTCTCT ATCACTGGTC GTGGTACTGT TGCTACCGGT | 420 |
| CGTATCGAGC GTGGCCGTAT CAAAGTTGGT GAGCCTGTTG AGATCGTAGG TCTGCAGGAG | 480 |
| TCTCCCCTGA ACTCTACCGT TACAGGTGTT GAGATGTTCC GCAAACCTCT CGACGAAGGT | 540 |
| GAAGCTGGTG ATAACGCCGG TCTCTCTCTC CGTGGTGTG AAAAAACACA GATCCGTCGC | 600 |
| GGTATGGTAA TCGTTAAACC CGGTTCCATC ACTCCGCACA CGGACTTCAA AGGCGAAGTT | 660 |
| TACGTACTGA GCAAAGACGA AGGTGGCCGT CACACTCCAT TCTTCAACAA ATACCGTCTT | 720 |
| CAATTCTACT TCCGTACAAC TGACGTTACA GGTGAAGTAG AACTGAACGC AGGAACAGAA | 780 |
| ATGGTTATGC CTGGTGATAA CACCAACCTG ACGTTAAAC TGATCCAACC GATCGCTATG | 840 |
| GAAAAAGGTC TGAAATTGCG GATCCGCGAA GGTGGCCGTA CCGTAGGTGC AGGA | 894 |

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

| | |
|---|-----|
| AATATGATTA CTGGTGGCGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC AGCAACAGAT | 60 |
| GGTCTTATGC CACAAACTCG TGAACACATC TTATTAGGTC GCCAAGTAGG TGTTCACATC | 120 |
| ATCATCGTAT TCTTAAACAA ATGCGACATG GTAGATGACG AAGAGTTATT AGAATTAGTC | 180 |
| GAAATGGAAG TTCGTGAATC TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC | 240 |

09589643-112001

| | |
|---|-----|
| GTACGTGGTT CAGCATTACA AGCGTTAAAC GGCCTAGCAG AATGGGAAGA AAAAATCCTT | 300 |
| GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT TGACCAACCG | 360 |
| TTCCTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC GTGGTACTGT AGTAACAGGT | 420 |
| CGTGTAGAAC GAGGTATTAT CCGTACAGGT GATGAAGTAG AAATCGTCGG TATCAAAGAT | 480 |
| ACAGCGAAAA CTACTGTAAC GGGTGTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT | 540 |
| GCAGGTGAAA ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT | 600 |
| CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC AGAAGTGTAC | 660 |
| GTATTATCAA AAGATGAAG TGGTGTCAT ACTCCATTCT TCAAAGGTTA CCGTCCACA | 720 |
| TTCTATTTC GTACAACAGA CGTGACTGGT ACAATCGAAT TACCAGAAGG CGTGGAAATG | 780 |
| GTAATGCCAG GCGATAACAT CAAGATGACA GTAAGCTTAA TCCACCAAT TGCATGGAT | 840 |
| CAAGGTTTAC GTTTCGAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 906 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

| | |
|--|-----|
| AACATGATCA CCGGTGCGCG GCAAATGGAC GGAGCGATT TGGTGTGTTT TGCAGCTGAT | 60 |
| GGCCCTATGC CTCAAAGTAG GGAGCATATC TTATTGTCTC GTCAGTAGG CGTGCCCTAC | 120 |
| ATCGTTGTTT TCTTAAACAA ACAAGACATG GTAGATGACC AAGAATTGTT AGAACTTGTA | 180 |
| GAAATGGAAG TGCGCGAATT GTTGAGCGCG TATGAATTTC CTGGCGATGA CACTCCTATC | 240 |
| GTAGCGGGTT CAGCTTTAAG AGCTTTAGAA GAAGCAAAGG CTGGTAATGT GGGTGAATGG | 300 |
| GGTGAAAAAG TGCTTAAACT TATGGCTGAA GTGGATGCCT ATATCCCTAC TCCAGAAGA | 360 |
| GACACTGAAA AAACCTTTCTT GATGCCGGTT GAAGATGTGT TCTCTATTGC GGGTAGAGGG | 420 |
| ACTGTGGTTA CAGGTAGGAT TGAAAGAGGC GTGGTGAAAG TAGGCGATGA AGTGAAATC | 480 |
| GTGGGTATCA GACCTACACA AAAAACGACT GTAACCGGTG TAGAAATGTT TAGGAAAGAG | 540 |
| TTGGAAGGAG GTGAAGCCGG CGATAATGTG GCGGTGCTTT TGAGAGGAAC TAAAAAGAA | 600 |

0999643-112001

(2) INFORMATION FOR SEQ ID NO: 159:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Micrococcus luteus*

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| AACATGATCA | CCGGCGCCGC | TCAGATGGAC | GGCGCGATCC | TCGTGGTCCG | CGTACCGAC | 60 |
| GGCCCCGATGG | CCCAGACCCG | TGAGCACGTG | CTCTGGCCC | GCCAGGTCCG | CGTGCCGGCC | 120 |
| CTGCTCGTGG | CCCTGAACAA | GTCGGACATG | GTGGAGGACG | AGGAGCTCCT | CGAGCGTGTC | 180 |
| GAGATGGAGG | TCCGGCAGCT | GCTGTCTCTC | AGGAGCTTCG | ACGTCGACGA | GGCCCCGGTC | 240 |
| ATCCGCACTT | CCGCTCTGAA | GGCCCTCGAG | GGCGACCCCC | AGTGGGTCAA | GTCCGTCGAG | 300 |
| GACCTCATGG | ATGCCGTGGA | CGAGTACATC | CCGGAACCCG | TGCGCGACAA | GGACAAAGCG | 360 |
| TTCTTGATCG | GATCGAGGA | CGTCTTCACG | ATCACCGGCC | GTGGACCCGT | GGTGACCGGT | 420 |
| CGCGCGAGCG | GCGGCACCCCT | GAAGATCAAC | TCCGAGGTGC | AGATCGTCGG | CATCCGCGAC | 480 |
| GTGCAGAAGA | CCACTGTAC | CGGCATCGAG | ATGTTCCACA | AGCAGCTCGA | CGAGGCCTGG | 540 |
| GCCGGCGAGA | ACTGCGGTCT | GCTCGTGCGC | GGTCTGAAGC | GCGACGACGT | CGAGCGCGGC | 600 |
| CAGGTGCTGG | TGGAGCCGGG | CTCCATCACC | CCGCACACCA | ACTTCGAGGC | GAACGCTTAC | 660 |
| ATCTGTCCA | AGSACGAGGG | TGGGCGTAC | ACCCCGTTCT | ACTGAACTA | CCGCGCGCAG | 720 |
| TTCTACTTCC | GCACCACCGA | CGTCAACGGC | GTCATCACGC | TGCCCGAGGG | CACCGAGATG | 780 |
| GTGATGCCCC | GCGACACCAC | CGAGATGTGC | GTGAGCTCA | TCCAGCCGAT | CGCCATGGAG | 840 |
| GAGGGCCTCG | GCTTCGCCAT | CCGCGAGGGT | GGCCGCACCG | TGGGCTCCGG | C | 891 |

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Mycobacterium tuberculosis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

| | |
|---|-----|
| AACATGATCA CCGCGCCGCG GCAGATGGAC GGTGCGATCC TGGTGGTCGC CGCCACCGAC | 60 |
| GGCCCGATGC CCCAGACCCG CGAGCACGTT CTGCTGGCGC GTCAAGTGGG TGTGCCCTAC | 120 |
| ATCTGGTAG CGCTGAACAA GGCCGACGCA GTGGACGACG AGGAGCTGCT CGAACTCGTC | 180 |
| GAGATGGAGG TCCGCGAGCT GCTGGCTGCC CAGGAATTGC ACGAGGACGC CCCGGTTGTG | 240 |
| CGGGTCTCGG CGCTCAAGGC GCTCGAGGGT GACGCGAAGT GGGTTGCCTC TGTGAGGAA | 300 |
| CTGATGAACG CGGTCGACGA GTCGATTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTT | 360 |
| CTGATGCCGG TCGAGGACGT CTTACCAATT ACCGGCCGCG GAACCGTGGT CACCGGACGT | 420 |
| GTGGAGCGCG GCGTGATCAA CGTGAACGAG GAAGTTGAGA TCGTCGGCAT TCGCCCATCG | 480 |
| ACCACCAAGA CCACCGTCAC CGGTGTGGAG ATGTTCCGCA AGCTGCTCGA CCAGGGCCAG | 540 |
| GCGGGCGACA ACGTTGGTTT GCTGCTGCGG GGCCTCAAGC GCGAGGACGT CGAGCGTGCG | 600 |
| CAGGTGTGCA CCAAGCCCGG CACCACCACG CCGCACACCG AGTTCGAAGG CCAGGTCTAC | 660 |
| ATCTGTGCCA AGGACGAGGG CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGACG | 720 |
| TTCTACTTCC GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCGGAGGG CACCGAGATG | 780 |
| GTGATGCCCG GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCGT CGCCATGGAC | 840 |
| GAAGGTCTGC GTTTCGCGAT CCGCGAGGGT GGCCGACCCG TGGGCGCCGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 891 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:

0908043-772001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| AATATGATCA | CAGGTGCTGC | ACAAATGGAT | GGAGCTATTC | TAGTGTGTTTC | AGCAACTGAT | 60 |
| AGTGTGATGC | CCCAAACCCG | CGAGCACATC | TTACTTGCCC | GCCAAGTAGG | GGTTCCTAAA | 120 |
| ATGGTAGTTT | TTCTAAACAA | GTGTGATATT | GCTAGTGATG | AAGAGGTACA | AGAACTTGTT | 180 |
| GCTGAAGAAG | TACGTGATCT | GTTAACCTCC | TATGGTTTTG | ATGGTAAGAA | CACTCCTATT | 240 |
| ATTTATGGCT | CAGCTTTAAA | AGCATTGGAA | GGTGATCCAA | AGTGGGAGGC | TAAGATCCAT | 300 |
| GATTTGATTA | AAGCAGTTGA | TGAATTGGATT | CCAACCTCTA | CACGTGAAGT | AGATAAACCT | 360 |
| TTCTTATTAG | CAATTGAAGA | TACGATGACC | ATTACTGGTA | GAGGTACAGT | TGTTACAGGA | 420 |
| AGAGTTGAAA | GAGGTGAACT | CAAAGTAGGT | CAAGAAGTTG | AAATTGTTGG | TTTAAACCA | 480 |
| ATTAGAAAAG | CAGTTGTTAC | TGGAATTGAA | ATGTTCAAAA | AGGAACCTGA | TTCAGCAATG | 540 |
| GCTGGTGACA | ATGCTGGGGT | ATTATTACGT | GGTGTGTAAC | GTAAGAAGT | TGAAGAGGTT | 600 |
| CAAGTTTTAG | CAAAACCAGG | CTCTATTAAA | CCGCACAAGA | AATTTAAAGC | TGAGATCTAT | 660 |
| GCTTTAAAGA | AAGAAGAAGG | TGGTAGACAC | ACTGGTTTTT | TAAACGGTTA | CCGTCTCAA | 720 |
| TTCTATTTC | GTACCACTGA | TGTAACCTGGT | TCTATTGCTT | TAGCTGAAAA | TACTGAATG | 780 |
| GTCTACCTG | GTGATAATGC | TTCTATTACT | GTTGAGTTAA | TGTCTCTAT | CGCTTGTA | 840 |
| AAAGGTAGTA | AGTTCTCAAT | TCGTGAAGGT | GGTAGAACTG | TAGGGGCAGG | C | 891 |

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 891 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| AACATGATTA | CGGGCGCCGC | ACAAATGSGAC | GGTGAATACC | TGGTATGTTC | TGCTGCCGAC | 60 |
| GGCCCTATGC | CGCAAACCG | CGAACACATC | CTGCTGGCCC | GTCAGTAGG | CGTACCTTAC | 120 |
| ATCATCTGTT | TCATGAACAA | ATGCGACATG | GTGACGATG | CCGAGCTGTT | CCAACTGGTT | 180 |
| GAAATGGAAA | TCCGCGACCT | GCTGTCCAGC | TACGACTTCC | CCGCGCAGCA | CTGCCCAGTC | 240 |

| | |
|--|-----|
| GTACAAGGTT CCGCACTGAA AGCCTTGGAA GCGGATGCCG CTTACGAAGA AAAATCTTC | 300 |
| GAACTGGCTA CCGCATTGGA CAGATACATC CCGACTCCCG AGCGTGCCGT GGACAAACCA | 360 |
| TTCTGTGTCG CTATCGAAGA CGTGTTCTCC ATTTCCGGCC GCGGTACCGT AGTCACGGC | 420 |
| CGTGTAGAGC GAGGTATCAT CCACGTTGGT GACGAGATTG AAATCGTCGG TCTGAAAGAA | 480 |
| ACCCAAAAA CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAG | 540 |
| GCGGCGGACA ACGTAGGCGT ATTGCTGCGC GGTACCAAAAC GTGAAGACGT AGAACGCGGT | 600 |
| CAGGTATTGG CCAAACGGGG TACTATCACT CCTCACACCA AGTTCAAAGC AGAAGTGTAC | 660 |
| GTATTGAGCA AAGAAGAGGG CGGCCCCCAT ACCCCGTTTT TCGCCAACTA CGTCCCCAA | 720 |
| TTCTACTTCC GTACCACTGA CGTAACCGGC ACGATTACTT TGGAAAAAGG TGTGGAATG | 780 |
| GTAATGCCGG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCTAT CGCTATGGAA | 840 |
| GAAGGTCTGC GCTTTGCGAT TCGCGAAGGC GCGCGTACCG TGGGTGCCGG C | 891 |

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rickettsia prowazekii*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

| | |
|--|-----|
| AATATGATAA CTGGTGCCGC TCAGATGGAT GGTGCTATAT TAGTAGTTTC TGCTGCTGAT | 60 |
| GGTCTATGCG CTCAACTAG AGAACATATA TTACTGGCAA AACAGGTAGG TGTACCTGCT | 120 |
| ATGGTAGTAT TTTTGAATAA AGTAGATATG GTAGATGATC CTGACCTATT AGAATTAGTT | 180 |
| GAGATGGAAG TAAGAGAATT ATTATCAAAA TATGGTTTCC CTGGTAATGA AATACCTATT | 240 |
| ATTAAAGGTT CTGCACITCA AGCTTTAGAA GGAACACCTG AAGGTGAAAA AGCTATTAAT | 300 |
| GAGTTAATGA ATGCAGTAGA TACGTATATA CCTCAGCCTA TAGAGCTACA AGATAAACCT | 360 |
| TTTTTAATGC CAATAGAGGA TGTATTTTCT ATTTTCAGGCA GAGGTACCGT TGTAAGTGGT | 420 |
| AGAGTGGAGT CAGGCATAAT TAAGGTGGGT GAAGAAATTG AAATAGTAGG TCTAAAAAAT | 480 |
| ACGCAAAAAA CGACTGTGAC AGGTGTAGAA ATGTTCAAGAA AATTACTTGA TGAAGGACAA | 540 |
| TCTGGAGATA ATGTCGGTAT ATTACTACGT GGTACAAAAA GAGAAGAAGT AGAAGAGGGA | 600 |

(2) INFORMATION FOR SEQ ID NO: 164:

- | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACATGATCA | CCGGTGCTGC | TCAGATGGAC | GGCGCGATCC | TGGTGTGTGC | TGCGACTGAC | 60 |
| GGCCCCGATG | CGCAGACCCG | TGAGCACATC | CTGCTGGGTC | GTCAGGTAGG | CGTTCCGTAC | 120 |
| ATCATCTGTT | TCCTGAACAA | ATGCGACATG | GTTGATGACG | AAGAGCTGCT | GGAACTGGTT | 180 |
| GAGATGGAAG | TTCGCGAACT | GCTGTCTCAG | TACGACTTCC | CGGGCGACGA | CACTCCGATC | 240 |
| GTTCTGTGTT | CTGCTCTGAA | AGCGCTGGAA | GGCGACGCAG | AGTGGGAAGC | GAAATCATC | 300 |
| GAACTGGCTG | GCTTCTTGGA | TTCTTATATT | CCGGAACCAG | AGCGTGCATG | TGACAAGCCG | 360 |
| TTCTGTCTGC | CGATCGAAGA | CGTATTCTCC | ATCTCCGGTC | GTGGTACCGT | TGTTACCGGT | 420 |
| CGTGTAGAGC | GCGGTATCAT | CAAAGTGGCG | GAAGAAGTTG | AAATCGTTGG | TATCAAAGAG | 480 |
| ACTCAGAAGT | CTACCTGTAC | TGGCGTTGAA | ATGTTCCGCA | AACTGCTGGA | CGAAGGCCGT | 540 |
| GCCGGTGAGA | ACGTAGGTGT | TCTGCTGCGT | GGTATCAAAC | GTGAAGAAAT | CGAACGTGGT | 600 |
| CAGGTACTGG | CTAAGCCGGG | CACCATCAAG | CCGCACACCA | AGTTCGAATC | TGAAGTGATG | 660 |
| ATTCTGTCCA | AAGATGAAGG | CGGCCGTCAT | ACTCCGTTCT | TCAAAGGCTA | CCGTCCGCAG | 720 |
| TTCTACTTCC | GTACTACTGA | CGTGACTGGT | ACCATCGAAC | TGCCGGAAGG | CGTAGAGATG | 780 |
| GTAATGCGCG | GCGACAACAT | CAAAATGGTT | GTTACCCTGA | TCCACCCGAT | CGCGATGGAC | 840 |
| GACGGTCTGC | GTTTCGCAAT | CCGTGAAGGC | GGCCGTACCG | TTGGCGCGGG | C | 891 |

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 881 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Shewanella putida*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| ATGATCACTG | GTGCTGCACA | GATGGACGGC | GCGATTCTGG | TAGTCGCTTC | AACAGACGGT | 60 |
| CCAATGCCAC | AGACTCGTGA | GCACATCCTG | CTTTCTCGTC | AGGTTGGCGT | ACCATTTCATC | 120 |
| ATCGTATTCA | TGAACAAATG | TGACATGGTA | GATGACGAAG | AGCTGTTAGA | GCTAGTTGAG | 180 |
| ATGGAAGTGC | GTGAACTGTT | ATCAGAATAC | GATTTCCCAG | GTGATGACTT | ACCGGTAATC | 240 |
| CAAGGTTTCA | CTCTGAAAGC | GCTAGAAGGC | GAGCCAGAGT | GGGAAGCAAA | AATCCTTGAA | 300 |
| TTAGCAGCGG | CGCTGGATTG | TTACATTCCA | GAACCACAAC | GTGACATCGA | TAAGCCGTTT | 360 |
| CTACTGCCAA | TCGAAGACGT | ATTCTCAATT | TCAGGCCGGT | GTACAGTAGT | AACAGGTCGT | 420 |
| GTTGAGCGTG | GTATTGTACG | CGTAGGCGAC | GAAGTTGAAA | TCGTTGGTGT | ACGTGCGACA | 480 |
| ACTAAGACAA | CGTGTACTGG | TGTAGAAATG | TTCCGTA AAC | TGCTTGACGA | AGGTCGTGCA | 540 |
| GGTGAGAACT | GTGGTATTTT | GTTACGTGGT | ACTAAGCGTG | ATGACGTAGA | ACGTGGTCAA | 600 |
| GTATTAGCGA | AGCCAGGTTT | AATCAACCCA | CACACTACTT | TTGAATCAGA | AGTTTACGTA | 660 |
| CTGTCAAAG | AAGAAGGTGG | TCGTACACAG | CCATTCTTCA | AAGGCTACCG | TCCACAGTTC | 720 |
| TACTTCCGTA | CAACTGACGT | AACCGGTACT | ATCGAACTGC | CAGAAGGCGT | AGAGATGGTA | 780 |
| ATGCCAGGGC | ATAACATCAA | GATGGTAGTG | ACACTGATTT | GCCCAATCGC | GATGGACGAA | 840 |
| GGTTTACGCT | TCGCAATCCG | TGAAGGCGGT | CGTACAGTGG | T | | 881 |

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 897 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Stigmatella aurantiaca*

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| AACATGATCA | CGGGCGCGGC | GCAGATGGAC | GGAGCGATTG | TGGTGGTGTG | CGCGGCCGAC | 60 |
| GGCCCCGATGC | CCCAGACGCG | TGAGCACATC | CTGCTGGCCA | GGCAGGTGGG | CGTGCCCTAC | 120 |
| ATCGTCGTCT | TCCTGAACAA | GGTGGACATG | CTGGACGATC | CGGAGCTGCG | CGAGCTGSGTG | 180 |
| GAGATGGAGG | TGCGCGACCT | GCTCAAGAAG | TACGAGTTCC | CGGGCGACAG | CATCCCCATC | 240 |
| ATCCCTTGCCA | GCGCGCTCAA | GGCGCTGGAG | GGAGACACCA | GCGACATCGG | CGAGGGAGCG | 300 |
| ATCCTGAAGC | TGATGGCGGC | GGTGGACGAG | TACATCCCGA | CGCCGCGAGC | TGCGACGGAC | 360 |
| AAGCCGTTCG | TGATGCCGGT | GGAAGACGTG | TTCTCCATCG | CAGGCCGAGG | AACGGTGGCG | 420 |
| ACGGGCGCAG | TGGAGCGCGG | CAAGATCAAG | GTGGGCGAGG | AAGTGGAGAT | CGTGGGGATC | 480 |
| CGTCCGACGC | AGAAGACGGT | CATCACGGGG | GTGGAGATGT | TCCGCAAGCT | GCTGGACGAG | 540 |
| GGCATGGCGG | GAGACAACAT | CGGAGCGCTG | CTGCGAGGCC | TGAAGCGCGA | GGACCTGGAG | 600 |
| CGTGGGCGAG | TGCTGGCGAA | CTGGGGGAGC | ATCAACCCGC | ACACGAAGTT | CAAGGCGCAG | 660 |
| GTGTACGTGC | TGTGGAAGGA | AGAGGGAGGG | CGGCACACGC | CGTTCTTCAA | GGGATACCGG | 720 |
| CCGCASTTCT | ACTTCCGGAC | GACGGACGTG | ACCGGAACGG | TGAAGCTGCC | GGACAACGTG | 780 |
| GAGATGGTGA | TGCCGGGAGA | CAACATCGCC | ATCGAGGTGG | AGCTCATTAC | TCCGGTCGCC | 840 |
| ATGGAGAAGG | AGCTGCCGTT | CGCCATCCGT | GAGGGTGGCC | GCACGGTGGG | CGCCGGC | 897 |

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACATGATCA | CTGGTCCGCG | TCAATGGAC | GGAGCTATCC | TTGTAGTTGC | TTCAACTGAT | 60 |
| GGACCAATCG | CACAAACTCG | TGAGCACATC | CTTCTTTCAC | GTCAGGTTGG | TGTTAAACAC | 120 |
| CTTATCGTGT | TCATGAACAA | AGTTGACCTT | GTTGATGACG | AAGAGTTGCT | TGAATTAGTT | 180 |
| GAGATGGAAA | TTCGTGACCT | TCTTTCAGAA | TACGATTTC | CAGGTGATGA | CCTCCAGTT | 240 |
| ATCCAAGGTT | CAGCTCTTAA | AGCTCTTGAA | GGCGACACTA | AATTGGAAGA | CATCATCATG | 300 |

| | |
|--|-----|
| GAATTGATGG ATACTGTTGA TTCATACATT CCAGAACCAG AACGCGACAC TGACAAACCA | 360 |
| TTGCTTCTTC CAGTCGAAGA CGTATTCTCA ATTACAGGTC GTGGTACAGT TGCTTCAGGA | 420 |
| CGTATCGACC GTGGTACTGT TCGTGTCAAC GACGAAATCG AAATCGTTGG TATCAAAGAA | 480 |
| GAAACTAAAA AAGCTGTTGT TACTGGTGTT GAAATGTTCC GTAAACAACCT TGACGAAGGT | 540 |
| CTTCGAGGAG ACAACGTAGG TATCCTTCTT CGTGGTGTTT AACGTGACGA AATCGAACGT | 600 |
| GGTCAAGTTA TTGCTAAACC AAGTTCAATC AACCCACACA CTAAATTCAA AGGTGAAGTA | 660 |
| TATATCCTTT CTAAAGACGA AGGTGGACGT CACACTCCAT TCTTCAACAA CTACCGTCCA | 720 |
| CAATTCTACT TCCGTACAAC TGACGTAACA GGTTCATCG AACTTCCAGC AGGTACAGAA | 780 |
| ATGGTTATGC CTGGTGATAA CGTGACAATC AACGTTGAGT TGATCCACCC AATCGCCGTA | 840 |
| GAACAAGGTA CTACTTTCTC AATCCGTGAA GGTGGACGTA CTGTTGGTTC AGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thiobacillus cuprinus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

| | |
|--|-----|
| AACATGATCA CCGGTGCGGC CCAGATGGAC GGC GCCATCC TGGTCGTGTC CGCCGCCGAC | 60 |
| GGCCCCATGC CCCAAACCCG CGAGCACATC CTGCTGGCGC GTCAGGTGGG CGTGCCCTAC | 120 |
| ATCATCGTGT TCCTCAACAA GTGCGACATG GTCGACGACG CCGAGCTGCT CGAACTCGTC | 180 |
| GAGATGGAAG TGC GCGAGCT GCTGTCCAAG TACGACTTCC CCGGTGACGA CACCCCCATC | 240 |
| ATCAAGGGCT CGGCCAAGCT GGCCTTCGAA GGC GACAAGG GCGAAGTGGG CGAAGGCGCC | 300 |
| ATTCTCAAGC TGGCCGAGGC CCTGGACACC TACATCCCCA CGCCGAGGCG GGCCGTGCGAC | 360 |
| GGCGCGTTC TCATGCCCCG GGAAGACGTG TTCTCCATCT CCGGGCGCGG CACGGTGGTC | 420 |
| ACCGGGCGTG TGGAGCGCGG CATCATCAAG GTCGGCGAGG AAATCGAGAT TGTCGGCCTC | 480 |
| AAGCCCACCC TCAAGACCAC CTGCACCGGC GTGGAATGT TCAGGAAGCT GCTCGACCAAG | 540 |
| GGCCAGGCCG GCGACAACGT CGGCATCTTG CTGCGCGGCA CCAAGCGCGA GGAAGTCGAG | 600 |
| CGCGGCCAGG TGCTGTGCAA ACCCGGCTCG ATCAAGCCCC ACACCCACTT CACCGCCGAG | 660 |

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| | |
|---|-----|
| GTGTACGTGC TGAGCAAGGA CGAGGGCGGC CGCCACACCC CCTTCTTCAA CAACTACCGC | 720 |
| CCGCAGTTCT ACTTCCGCAC CACCGACGTC ACCGGCGCCA TCGAACTGCC CAAGGACAAG | 780 |
| GAAATGGTCA TGCCCCGCCA TAATGTGAGC ATCACCCTCA AGCTCATCGC CCCCATCGCC | 840 |
| ATGGAAGAAG GCCTGCGCTT GCCTATCCGC GAAGGCGGCC GCACCGTCGG CGCCGGC | 897 |

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Treponema pallidum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

| | |
|---|-----|
| AATATGATCA CGGGTGTGC GCAGATGGAC GGTGGTATTC TCGTCGTGC TGCCTGAC | 60 |
| GGCGTTATGC CACAGACGAA GGAGCATCTT CTGCTCGCCC GTCAGGTTGG TGTTCCCTCC | 120 |
| ATCATGTTT TTTGAACAA GGTGATTG GTTGATGATC CTGAGTTGCT AGAGCTGGT | 180 |
| GAAGAAGAGG TCGGTGATGC GCTTGCTGGA TATGGGTTTT CGCGTGAGAC GCCTATCGTC | 240 |
| AAGGGGTCTG CGTTTAAAGC TCTGCAGGAT GGCCTTCCC CGGAGGATGC AGCTTGTATT | 300 |
| GAGGAATGCT TTGCGCCAT GGATTCCTAC TTGAAGACC CAGTCGTGA CGACGCAAGA | 360 |
| CCTTCTTGCT TCTCTATCGA GGATGTGTAC ACTATTCTG GCGTGGTAC CGTTGTACAG | 420 |
| GGGCGCATCG AATGTGGGTT AATTAGTCTG AATGAAGAGG TCGAGATCGT CGGGATTAAG | 480 |
| CCCACTAAGA AAACAGTGGT TACTGGCATT GAGATGTTA ATAAGTTGCT TGATCAGGGA | 540 |
| ATTGCAGGTG ATAACGTGGG GCTGCTTTTG CGCGGGGTGG ATAAAAAGA GGTGAGCGC | 600 |
| GGTCAGGTGC TTTCTAAGCC CGGTTCTATT AAGCCACACA CCAAGTTTGA GGCAGCATC | 660 |
| TACGTGCTCT CTAAGGAAGA GGTGGCCGT CACAGTCCTT TTTTCAAGG TTATCGTCCG | 720 |
| CAGTTTATT TTAGAATACT TGACATTACC GGTACGATT CTCTCTCTGA AGGGGTAGAC | 780 |
| ATGTTGAAGC CGGGGGATAA CACCAAGATT ATAGGTGAGC TCATCCACCC GATAGCTATG | 840 |
| GACAAGGGTC TGAAGCTTGC GATTCTGTAA GGGGGGCGCA CTATTGCTTC TGGT | 894 |

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

(2) INFORMATION FOR SEQ ID NO: 171:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

| | |
|---|-----|
| AACATGATTA CAGGTGCTGC TCAATGGAT GGCSCGATTC TTGTTGTTTC TGCSCGGAT | 60 |
| GGCCCCATGC CCCAAACTAG GGAGCACATT CTTCTTTCTC GACAAGTAGG CGTTCCTTAC | 120 |
| ATCGTGGTTT TCTTGAACAA AGAAGATATG GTTGATGACG CTGAGCTTCT TGAGCTTGTT | 180 |
| GAAATGGAAG TTAGAGAACT TCTTAGCAAC TACGACTTCC CTGAGATGA CACTCCTATC | 240 |
| GTTGCAGGTT CCGCTCTTAA AGCTCTTGAA GAGGCTAACG ACCAGGAAAA TGTGCGCGAG | 300 |
| TGGGGCGAGA AAGTATTGAA GCTTATGGCT GAGGTTGACC GATATATTCC TACGCCTGAG | 360 |
| CGAGATGTGG ATAAGCCTTT CCTTATGCCT GTTGAAGACG TATTCTCCAT CGCGGGTCGT | 420 |
| GGAACCGTTG TGACAGGAAG AATTGAAAGA GCGGTGTTA AAGTCGGTGA CGAAGTAGAA | 480 |
| ATCGTTGGTA TCCGAAACAC ACAAAAAACA ACCGTAAC TGCGTTGAGAT GTTCCGAAAA | 540 |
| GAGCTCGACA AGGGTGAGGC GGGTGACAAC GTTGGTGTTT TTTTGAAGG CACCAAGAAA | 600 |
| GAAGATGTTG AGAGAGGTAT GGTTCCTTGT AAAATAGGTT CTATCACTCC TCACACTAAC | 660 |
| TTTGAAGGTG AAGTTTACGT TCTTTCCAAA GAGGAAGGCG GACGACACAC TCCATTCTTC | 720 |
| AATGGATACC GACCTCAGTT CTATGTTAGA ACTACAGACG TTACCGGTTT TATCTCTCTT | 780 |
| CCTGAGGGCG TAGAGATGGT TATGCCTGGT GACAACGTTA AGATCAATGT TGAGCTTATC | 840 |
| GCTCCTGTAG CCCTCGAAGA GGAACACGA TTCGCGATCC GTGAAGGTGG TCGAACCGTT | 900 |
| GGTGCGGGT | 909 |

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:12
- (D) OTHER INFORMATION:/note= "n = inosine"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:18
- (D) OTHER INFORMATION:/note= "n = inosine"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TARTCNGTRA ANGCTCNAC RCACAT

26

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

TCTTTAGCAG AACAGGATGA A

21

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GAATAATTCC ATATCCTCCG

20

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